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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) **Abstract:** A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S.provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_HEART.txt, created 24 January 2001, having 20,186,946 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert *et al.*, *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick *et al.*, *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams *et al.*, *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999), there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin *et al.*, *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher *et al.*, *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu *et al.*, *Genet. Eng.* 16:241-53 (1994); Uberbacher *et al.*, *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev *et al.*, *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev *et al.*, *Ismb* 5:294-302 (1997); and GENESCAN, Burge *et al.*, *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset *et al.*, *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari *et al.*, *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. *Reviewed in* Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon *et al.*, *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi *et al.*, *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single exon genes, *i.e.*, lack introns, Lopez *et al.*, *RNA* 5:1135-1137 (1999); Goffeau *et al.*, *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 9,981 - 19,771, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 9,980.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7, preferably at least 10^8, more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30})("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, *e.g.*, syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, *e.g.*, Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis *et al.*, Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, http://cmgm.stanford.edu/pbrown/mguide/index.html), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived – either directly or indirectly – from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 - 5% – have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, *Reviewed in* Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis *et al.*, or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra,* Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, *etc.*, and can be provided in dry (*e.g.*, lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query — including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (*e.g.*, a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, *e.g.*, by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (*e.g.*, mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in the United States and other developed countries. In developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for genetic causes of cardiovascular diseases. For example, studies by Allayee et al., Am. J. Hum. Genet. 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., Am. J. Hum. Genet. 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., Proc. Nat. Acad. Sci. 89: 708-712 (1992) and Rotter et al., Am. J. Hum. Genet. 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., supra, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., Mutat 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL), that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic kidney disease, medullary thyroid cancer, pheochromocytoma, and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor receptor-2, and "-adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone, encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular block, familial sinus node disease, progressive cardiac conduction defect, and familial cardiomyopathy. Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3. Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects have been identified. For example, Greenberg et al., Am. J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al., Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis *et al.* – each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski *et al.*, "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz *et al.*, "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss *et al.*, "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton *et al.*,"Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer *et al.*, "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," Proc. Natl. Acad. Sci. USA 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon *et al.*, "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou *et al.*, "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang *et al.*, "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney *et al.*, "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf *et al.*, "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi *et al.*, "*In vivo* Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents — whether in lead compound discovery or in subsequent screening of lead compound derivatives — the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al., Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, *etc.*, required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis *et al.* For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_0t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^{3}H, ^{32}P, ^{33}P, ^{35}S, ^{125}I, ^{131}I; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR®

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis *et al.*

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis *et al.*

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (*e.g.*, HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan *et al.* (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at http://www-genome.wi.mit.edu/cgi-bin/primer/). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish *et al.*, *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis

Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA$^+$ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal – where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) – 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (*i.e.*, degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than 1e-30 ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca^{2+} binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1□ (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai *et al.*, *Genomics* 49(2):283-89 (1998))(AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes *et al.*, *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ±0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom): red = kallistatin protease inhibitor (P29622); purple = plasma serine protease inhibitor (P05154); turquoise = α1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more that a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO:. of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (*i.e.*, highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (*i.e.*, lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (*e.g.*, those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (*i.e.*, 1×10^{-5}) and 1e-100 (*i.e.*, 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, *e.g.*, less than about 1e-100 – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
442	10386	20209	4.41				
871	10797	20647	17.08				
1029	10947		2.14				
1280	11188	21039	7.97				
1597	11501	21361	1.87				
1619	11523	21381	4.97				
1694	11596	21467	1.01				
1715	11616	21485	0.95				
1721	11622	21491	7.46				
1848	11744	21620	0.98				
1935	11830	21713	3.03				
2119	12008	21907	2.62				
2233	12118	22020	2.34				
3149	13074	22875	3.7				
3403	13320	23121	1.52				
3471	13387	23192	8.97				
3513	13429		0.87				
3607	13521	23309	0.99				
4102	14002	23781	1.71				
4164	14064	23838	5.94				
4184	14084	23858	0.89				
4184	14084	23859	0.89				
4242	14141		1.03				
4730	14616	24402	1.76				
4779	14663		0.78				
4976	14851	24617	5.08				
4988	14863	24629	2.07				
5217	15140	24834	1.92				
5217	15140	24835	1.92				
5328	15248		5				
5436	15356		5.89				
5483	15248		4.9				
5509	15427	25490	2.9				
5668	19451	25678	1.6				

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5690	15599	25700	1.41				
5863	15769		1.84				
6382	16244	26404	1.61				
6382	16244	26405	1.61				
6697	16577	26769	1.29				
6942	16820	27012	1.3				
7494	17364	27569	3.68				
7684	17534	27758	1.26				
8070	17961		3.7				
8219	19472	28355	2.31				
8390	18266		2.84				
8666	18555	28840	2.91				
8757	17906	28150	1.73				
8757	17906	28151	1.73				
8792	18606		2.19				
9464	19094		1.62				
9760	19280	25230	2.11				
5691	15600	25701	13.31	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6669	16549	26745	1.54	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
7955	17805	28046	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
7955	17805	28047	1.32	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIH polypeptide 2 (Gtf2h2) genes, complete cds
2631	12499	22389	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22390	2.72	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2893	12820	22612	5.91	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
7206	17083	27271	2.97	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5239	15163	24932	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24933	2.07	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5678	15587	25687	5.51	8.9E+00	BE971606.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754	25871	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
5848	15754	25872	1.71	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
433	10378	20199	1.76	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
7439	16452	26642	3.68	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
8509	18381		2.31	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6346	16209		2.07	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
6868	16747	26940	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6868	16747	26941	1.53	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	25531	2.58	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
7085	16962	27155	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
7085	16962	27156	3.83	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
2947	12874	22672	4.2	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17386		8.48	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8690	18577	28860	3.26	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
7735	17585	27809	2.98	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8575	18443	28712	1.85	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MSI3
6818	16697	26889	2.72	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
7925	17775	28015	1.3	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
6614	16494	26680	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
6614	16494	26681	1.45	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291860 5'
7277	17154		1.47	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
7863	17713	27957	3.82	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
7796	17646	27881	2.1	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7796	17646	27882	2.1	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18344		2.17	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
7296	17172	27372	8.32	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
7616	17467	27686	1.44	6.2E+00	AY010901.1	NT	Schizophyllum commune unknown mRNA
5928	15833	25956	7.16	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3479	13395		0.81	5.8E+00	7661557	NT	Homo sapiens DESC1 protein (DESC1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8770	17919	28166	2.44	5.6E+00	Q55276	SWISSPROT	LYCOPENE BETA CYCLASE
8769	17918	28165	2.65	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
8967	18773		1.94	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
6593	16473		1.62	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
7769	17619	27849	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
7769	17619	27850	1.44	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4675	14561	24354	1.54	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6710	16590		4.04	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8899	18708	29003	3.21	5.3E+00	Q27905	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
7655	17505	27730	1.21	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
7959	17809	28050	3.06	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
8610	18477	28749	10.53	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
3972	13879		9.43	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
6970	16847		5.01	4.8E+00	AW750067.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
286	10251	20071	2.03	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
287	10251	20071	1.92	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3236	13160	22958	4.01	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6576	16434	26617	1.48	4.6E+00	U67569.1	NT	Methanococcus jannaschii section 111 of 150 of the complete genome
8881	18693	28986	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3003	12931	22723	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3003	12931	22724	0.96	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
5764	15671		1.55	4.4E+00	X13414.1	NT	Murine I gene for MHC class II(Ia) associated invariant chain
6398	16259	26420	2.01	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
8235	18116	28368	7.49	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5387	15306		2.92	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
6060	16043	26186	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6060	16043	26187	1.57	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
7182	17059	27249	5.45	4.2E+00	AI809013.1	EST_HUMAN	wf67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6517	16376	26553	7.65	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6577	16435	26618	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
6577	16435	26619	3.31	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6617	16497	26684	2.95	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
7576	17427	27641	2.31	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
8259	18139		2.89	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
8339	18216		12.46	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
9672	19231	25241	1.86	4.1E+00	P47876	SWISSPROT	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDING PROTEIN 1)
6266	16131	26285	1.37	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8768	17917	28164	2.17	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
8835	18648	28934	3.34	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8835	18648	28935	3.34	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3459	13375	23181	3.89	3.9E+00	X64518.1	NT	N.tabacum chitinase gene 50 for class I chitinase C
4226	14124		0.99	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5471	15391	25454	2.47	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5471	15391	25455	2.47	3.9E+00	BE814357.1	EST_HUMAN	MR0-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6108	16002	26140	4.46	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
6355	16218	26379	4.68	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6840	16719	26913	2.32	3.9E+00	X65865.1	NT	X.laevis mRNA for M4 muscarinic receptor
8695	17879	28120	3.09	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
8715	18532	28816	5.58	3.9E+00	AA661489.1	EST_HUMAN	nr18a12.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
2588	12459		2.4	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6911	16789	26982	1.18	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
3936	13845	23622	10.09	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
8730	18586	28872	2.13	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
8730	18586	28873	2.13	3.7E+00	BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
578	10516	20322	2.1	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
7022	16899	27090	3.66	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
7022	16899	27091	3.66	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		3.76	3.6E+00	M96795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
3209	13133	22934	1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1496	11400	21260	3.57	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
2532	12406	22298	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6354	16217	26378	2.41	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17739	27982	3.17	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8818	18631	28919	1.92	3.4E+00	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
5036	14908	24679	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14908	24680	1.41	3.3E+00	7662155	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
492	10435	20248	1.39	3.2E+00	X96422.1	NT	D.rerio zp-50 POU gene
3938	10435	20248	0.79	3.2E+00	X98422.1	NT	D.rerio zp-50 POU gene
5439	15359	25415	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5439	15359	25416	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5808	15713	25825	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5808	15713	25826	2.06	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6569	16427	26609	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6569	16427	26610	2.35	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7221	17098		6.33	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
7491	17361	27567	1.17	3.2E+00	M36383.1	NT	S.cerevisiae threonine deaminase (ILV1) gene, complete cds
7837	17687	27932	1.69	3.2E+00	AB016081.2	NT	Oryzias latipes OlGC6 gene for guanylyl cyclase C, complete cds
9089	18863		4.32	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5582	15497	25574	2.42	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7000	16877	27067	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7000	16877	27068	4.35	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
7334	17238		3.8	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
7920	17770	28009	4.78	3.1E+00	P49365	SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
8759	17908		3.78	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8774	18591		3.35	3.1E+00	S56660.1	NT	retinoic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2807	12737	22536	1.06	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5273	15195	24970	1.63	3.0E+00	X53096.1	NT	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease
6245	16111		9.6	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7164	17041		1.45	3.0E+00	X67838.1	NT	B.napus DNA for myrosinase
8374	18251	28501	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
8374	18251	28502	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLATE CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLATE CYCLASE 2) (ROS-GC2) (GUANYLATE CYCLASE F) (GC-F)
1964	11858	21747	2.56	2.9E+00	AE002225.2	NT	Chlamydophila pneumoniae AR39, section 53 of 94 of the complete genome
6129	15976	26112	1.63	2.9E+00	Z36879.1	NT	F.pringlei gdcsPA gene for P-protein of the glycine cleavage system
6282	16146	26300	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6282	16146	26301	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6410	16271	26433	5.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11346	21212	5.79	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1616	11519		3.12	2.8E+00	AL161652.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6325	16188	26350	4.78	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
230	10199	20012	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
230	10199	20013	4.63	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5408	15327	25377	1.75	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
7185	17062		2.21	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7996	17846		2.16	2.7E+00	BE063527.1	EST_HUMAN	CM0-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
4576	14467	24253	4.35	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5405	15324	25373	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5405	15324	25374	1.97	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6533	16391		5.42	2.6E+00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
6696	16576	26767	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
6696	16576	26768	1.2	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
7567	17418	27634	2.95	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7927	17777		1.52	2.6E+00	9055193	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19649		2.31	2.6E+00	11419220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1448	11353	21216	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1448	11353	21217	2.08	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5552	15468	25537	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5552	15468	25538	2.33	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25537	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15468	25538	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6561	16419	26598	1.34	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7264	17141	27334	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9086	18861		2.26	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
2980	12907	22707	0.86	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4816	14699	24485	7.62	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
5657	15569	25664	4.19	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
6733	16613	26802	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6733	16613	26803	2.14	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
6780	16659		2.63	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
7026	16903		1.71	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7125	17002	27194	9.45	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17621	27853	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7771	17621	27854	2.5	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7820	17670	27911	2.18	2.4E+00	X92511.1	NT	H:sapiens CTGF gene and promoter region
7881	17731		6.49	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
7914	17764	28002	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
7914	17764	28003	1.67	2.4E+00	BE326702.1	EST_HUMAN	hr63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
8428	18302	28558	1.77	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFKD operon and downstream
8665	18554	28839	2.52	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1233	11140	20992	9.36	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4031	13934		1.28	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6408	16269	26431	2.22	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
6479	19766		2.3	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	16431	26613	1.53	2.3E+00	X60265.1	NT	M.mazei dnaK and dnaJ genes homologues coding for DnaK and DnaJ
7289	17165	27364	1.81	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 4) (FUCT-IV)
8988	18793	29083	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
8988	18793	29084	2.6	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9304	19002	25333	4	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
9936	19405		1.37	2.3E+00	AF281862.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5276	15198	24973	10.08	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5276	15198	24974	10.08	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5696	15605	25707	9.06	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
5835	15741	25853	3.3	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
5978	15882	26005	2.89	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6155	15113		3.14	2.2E+00	AA594574.1	EST_HUMAN	nl95b02.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
6486	16344	26514	51.56	2.2E+00	AA449012.1	EST_HUMAN	zx05g10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7381	17250		11.83	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
7518	19468		2.1	2.2E+00	Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A
7783	17633	27865	1.56	2.2E+00	AI290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7783	17633	27866	1.56	2.2E+00	AI290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
7812	17662	27902	2.28	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4075391 5'
7975	17825	28066	2.88	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
8739	17888	28132	4.5	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
8889	18700	28995	4.67	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
557	12670	20304	6.81	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3539	13455		1.19	2.1E+00	AW449366.1	EST_HUMAN	UI-H-BI3-aki-e-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6074	16057	26206	3.72	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6195	15955	26087	4.7	2.1E+00	N29575.1	EST_HUMAN	yy08a10.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654 TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
6948	16826		1.99	2.1E+00	AU123630.1	EST_HUMAN	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1178	11089	20934	1.23	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1178	11089	20935	1.23	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1313	11219	21076	1.43	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na+,K+-ATPase beta 1 subunit mRNA, complete cds
1557	11462		3.13	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2102	11991	21890	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
2102	11991	21891	4.6	2.0E+00	Z78279.1	NT	R.norvegicus mRNA for collagen alpha1 type I
4011	13917	23692	2.09	2.0E+00	AW664496.1	EST_HUMAN	hl13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
4011	13917	23693	2.09	2.0E+00	AW664496.1	EST_HUMAN	hl13c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
6678	16558	26751	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26752	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6678	16558	26753	3.8	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7170	17047	27237	3.3	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
9629	19613	24998	5.81	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5437	15357	25412	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
5437	15357	25413	4.67	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (Itpr1), mRNA
6047	15950		2.27	1.9E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
6927	16805	26999	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6927	16805	27000	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7032	16909		3.36	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
7156	17033		1.86	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
3054	12981	22773	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	13009	22799	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3082	13009	22800	4.48	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5577	15492		2.22	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	15620	25723	1.9	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6043	15946	26078	1.3	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7140	17017	27210	2.09	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
7293	17169	27369	1.21	1.8E+00	R31042.1	EST_HUMAN	yh72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
7899	17749		3.29	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
8998	18801		3.76	1.8E+00	P36062	SWISSPROT	HYPOTHETICAL 75.5 KD PROTEIN IN SDH1-CIM5/YTA3 INTERGENIC REGION

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9428	19584		4.01	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9504	19119		2.4	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
9968	19429		1.34	1.8E+00	BF316805.1	EST_HUMAN	601903309F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135586 5'
1092	11008	20849	1.92	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013	3.25	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202	22101	1.02	1.7E+00	AI141067.1	EST_HUMAN	oz43h05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4356	14252	24037	0.84	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369	25424	1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5448	15369	25425	1.48	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5664	15575	25673	3.58	1.7E+00	Q9TTR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
7014	16891		1.29	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
7282	19467	27355	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
7282	19467	27356	2.15	1.7E+00	O60479	SWISSPROT	HOMEOBOX PROTEIN DLX-3
8874	18686	28977	1.78	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9384	19044	25306	1.37	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.t1 MSR1 repetitive element ;
9860	19351	25185	2.26	1.7E+00	AI198573.1	EST_HUMAN	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.t1 L1 repetitive element ;
1989	11882	21775	16.73	1.6E+00	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21783	3.61	1.6E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	11896	21788	1.96	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2238	12122		1.48	1.6E+00	X98373.1	NT	B.napus gene encoding endo-polygalacturonase
2931	12858	22658	2.52	1.6E+00	W58426.1	EST_HUMAN	zd25f01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
3946	13854		5.14	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4255	14154	23928	1.44	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4255	14154	23929	1.44	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5016	14890	24657	3.14	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5016	14890	24658	3.14	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5558	15474	25546	2.19	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6296	16160	26317	2.64	1.6E+00	BE697267.1	EST_HUMAN	RC0-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6681	16561		1.21	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
6881	16760	26958	3.56	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
7444	19465	26646	1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
7444	19465	26647	1.3	1.6E+00	X52046.1	NT	M.musculus COL3A1 gene for collagen alpha-I
7611	17462	27679	1.29	1.6E+00	T41290.1	EST_HUMAN	ph6b6_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6b6_19/1TV
7852	17702	27946	1.25	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
7852	17702	27947	1.25	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-d07 LT0016 Homo sapiens cDNA
8217	15520	25601	5.86	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (TgaseI) gene, promoter region
8944	18752	29047	3.25	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
9902	19379		1.65	1.6E+00	AV764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
30	10017	19812	4.29	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.5E+00	AE002201.2	NT	Chlamydophila pneumoniae AR39, section 32 of 94 of the complete genome
605	10541		1.79	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metargidin) (Adam15), mRNA
2359	12239	22135	2.46	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2468	12344	22237	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis·1 (Tiam1), mRNA
3099	12239	22135	2.22	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.82	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5856	15762	25880	2.71	1.5E+00	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
6230	16096		1.42	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
6250	16116	26268	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
6250	16116	26269	29.13	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7671	17521	27747	7.56	1.5E+00	BF376754.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
7782	17632		1.71	1.5E+00	BF337944.1	EST_HUMAN	602035771F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183865 5'
7856	17706	27951	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
7856	17706	27952	1.96	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
8702	18520	28802	3.91	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243_s1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P243 3'
8828	18641		10.73	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
9223	18946		1.5	1.5E+00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ap2), mRNA
9596	19178		2.89	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9690	19243		1.42	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxygenase (Alox5), mRNA
27	10014	19808	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
27	10014	19809	1.28	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2231	12116		0.95	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2286	12169		9.38	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2634	12501	22394	1.63	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12608	22500	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	12608	22501	3.29	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12962	22755	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3034	12962	22756	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome
3291	13213		0.87	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4162	14062	23835	1.09	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4162	14062	23836	1.09	1.4E+00	AW900465.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4482	14376		1.53	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5137	15004		0.8	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5301	15222	25026	1.51	1.4E+00	AW054976.1	EST_HUMAN	wt45g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5394	15313		5.17	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
5796	15702	25812	2.39	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5802	19765		4.9	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5860	15766	25884	2.71	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
5860	15766	25885	2.71	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6318	16181	26341	1.86	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7107	16984		5.21	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
7256	17133	27325	1.88	1.4E+00	R20459.1	EST_HUMAN	yg33f12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34345 5'
7303	17179	27381	3.37	1.4E+00	BE064667.1	EST_HUMAN	RC1-BT0313-301299-012-f05 BT0313 Homo sapiens cDNA
8420	18294	28548	1.94	1.4E+00	AA195528.1	EST_HUMAN	zr36e09.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element ;
8556	18426	28695	4.97	1.4E+00	AB006682.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
8709	18526	28808	5.15	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8709	18526	28809	5.15	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
8727	18583	28867	2.68	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8727	18583	28868	2.68	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9221	19604		1.34	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
558	10498		1.67	1.3E+00	Z73640.1	NT	M.mucedo gene encoding 4-Dihydromethyl-trisporate dehydrogenase
884	10810	20659	2.74	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1113	11028		16.5	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1275	11183	21033	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1275	11183	21034	10.9	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1334	11241		1.62	1.3E+00	U61730.2	NT	Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1593	11497		2.09	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2196	12083		2.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2503	12378		2.19	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2909	12835	22632	1.12	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
3547	13463	23258	1.03	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4502	12835	22632	0.82	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
4964	14839	24607	0.98	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
4964	14839	24608	0.98	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25674	7.76	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
5665	15576	25675	7.76	1.3E+00	AW362834.1	EST_HUMAN	PM0-CT0289-291199-004-f08 CT0289 Homo sapiens cDNA
5864	15770	25889	1.33	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6828	16707	26901	1.25	1.3E+00	AJ009912.1	NT	Sus scrofa pip gene
6917	16795	26988	3.06	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
7054	16931		1.55	1.3E+00	9910247	NT	Homo sapiens GL004 protein (GL004), mRNA
7480	17350		5.44	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
7487	17357	27560	2.31	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
7487	17357	27561	2.31	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
7574	17425	27639	1.45	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
7620	17471	27690	1.27	1.3E+00	AI927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
7676	17525	27751	4.9	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
7866	17716	27961	1.6	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
7874	17724	27968	1.39	1.3E+00	M29953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
8078	17969		4.3	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
8277	18157	28398	2.34	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8299	18178	28424	2.23	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
8646	18510		1.81	1.3E+00	AW274791.1	EST_HUMAN	xp09e03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739868 3'
8826	18639	28923	2.82	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8895	18705	28999	2.71	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9kB fragment
9362	19033		2.35	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
9533	19139	25263	3.24	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'
9544	19499		2.68	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
634	10571	20384	8.14	1.2E+00	AA676246.1	EST_HUMAN	zi22d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
806	10735	20578	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
806	10736	20579	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
806	10735	20580	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
860	10786		2.19	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1145	11058	20901	5.53	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1963	11857	21746	1.05	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22789	0.95	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22851	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	13053	22852	5.41	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13172		2.9	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3312	13233		0.99	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
3650	13564	23350	7.28	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
3904	13814	23598	1.49	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4298	14196	23981	1.39	1.2E+00	6980951	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glra2), mRNA
4371	14267		1.64	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4422	14316	24102	1.26	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4460	14354	24145	1.82	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4485	14379		5.44	1.2E+00	Y09200.1	NT	T.pinnatum chloroplast rbcL gene, partial
4584	13233		0.94	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds.
5409	15329	25379	1.96	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5739	15647	25753	2.47	1.2E+00	X74885.1	NT	D.hydei ay1 repeat cluster DNA, fragment D
5769	15676	25783	3.28	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5798	15704	25815	1.87	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
5798	15704	25816	1.87	1.2E+00	X89084.1	NT	C.glutamicum pta gene and ackA gene
5823	15729	25841	32.83	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
5918	15823	25949	1.82	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6139	15986	26121	2.55	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6369	19463	26392	1.9	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cdA Homo sapiens cDNA clone cdAAFH03 5'
6508	16367	26544	2.4	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
6984	16861	27055	3.45	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7218	17095	27285	1.74	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
7407	17274	27480	3.08	1.2E+00	Z32850.1	NT	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27601	1.8	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
7711	17561	27786	3.28	1.2E+00	X56832.1	NT	H.sapiens ENO3 gene for muscle specific enolase
8653	18542	28826	2.03	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0264-161199-001-d01 ST0264 Homo sapiens cDNA
8689	18576		23.47	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
8752	17901	28145	4.87	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
9114	18877	28787	2.5	1.2E+00	AF065398.1	NT	Mus musculus 60 kDa ribonucleoprotein SSA/Ro gene, complete cds
9330	19572	25067	15.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9349	19025		1.49	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
456	10400	20217	1.13	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1726	11627	21496	1.39	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1857	11753	21628	0.92	1.1E+00	AW575889.1	EST_HUMAN	UI-HF-BR0p-ajk-f-02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
3288	13209	23009	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	13209	23010	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	13358	23165	0.93	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3510	13426		1.26	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	13447	23244	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3657	13571	23357	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3657	13571	23358	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3678	13592	23378	17.81	1.1E+00	5729757	NT	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA
3862	13773	23565	0.99	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4122	14022		5.89	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
4860	14740	24520	1.18	1.1E+00	L23195.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
4921	14800	24573	2.92	1.1E+00	U18466.1	NT	African swine fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4999	14874	24638	1.16	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5249	15172	24945	1.57	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5449	15370	25426	12.04	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5460	15380	25440	1.29	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6422	16283	26444	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	16283	26445	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6436	16296	26458	7.53	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6728	16608	26799	3.22	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
7658	17508	27733	1.65	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
7716	17565	27791	4.39	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27815	20.08	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
8043	17934	28182	2.65	1.1E+00	11067364	NT	*Homo sapiens KIAA0626 gene product* (KIAA0626), mRNA
8090	17981		3.41	1.1E+00	AF068942.1	NT	Klebsormidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8447	13426		5.73	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
8450	18323	28581	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8450	18323	28582	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
8662	18551	28835	4.73	1.1E+00	AI809699.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
9300	18999		4	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19056	25310	2.13	1.1E+00	AF216696.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
9523	19570		1.54	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
92	10077		3.49	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
108	10089	19904	1.14	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threoine kinase, complete cds
412	10358		2.16	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
562	10502	20308	1.14	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
661	10595	20413	4.51	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
663	10597		0.95	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1364	12692		1.04	1.0E+00	X80416.1	NT	V.carteri Algal-CAM mRNA
1722	11623	21492	1.32	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2435	12312	22208	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2651	12518	22408	1.09	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Smn), neuronal apoptosis inhibitory protein-rs6 (Naip-rs6), and neuronal apoptosis inhibitory protein-rs3 (Naip-rs3) genes, complete cds
2846	12774	22561	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	12774	22562	3.48	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	12865		0.99	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3162	13087	22891	1.17	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:C42D8.3 CE04204 ;contains element MER22 MER22 repetitive element ;
3327	13247		0.81	1.0E+00	AF222761.1	NT	Rattus norvegicus neuromedin U precursor (NmU) gene, exons 5 and 6
3548	10077		1.15	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3627	13541	23328	1.44	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
3978	13885	23660	0.86	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4178	14078		0.79	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4815	14698		0.88	1.0E+00	U75741.1	NT	Taenia ovis 45W antigen (ToW4) gene, complete cds
4951	14828		0.88	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5139	15006	24777	0.87	1.0E+00	AJ223978.1	NT	Bacillus subtilis 42.7kB DNA fragment from yvsA to yvqA
5228	15152	24919	2.49	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5568	15484	25557	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5568	15484	25558	4.31	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5719	15626	25729	4.82	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
5720	15627	25730	1.39	1.0E+00	AW452782.1	EST_HUMAN	UI-H-BI3-alx-d-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
5908	15814	25939	2.21	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6417	16279		8.43	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6537	16395	26574	1.34	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
6546	16404	26583	5.99	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868791 3'
6641	16521	26713	1.71	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6641	16521	26714	1.71	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
6734	14828		1.38	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6861	16740	26932	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6861	16740	26933	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6967	19466		2.01	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e06 HT0229 Homo sapiens cDNA
7064	16941	27133	1.9	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
7339	17207	27405	1.76	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
7460	17320	27526	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
7460	17320	27527	1.28	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
7544	17395	27607	2.03	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
7546	17397	27609	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
7546	17397	27610	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
7916	17766	28005	2.83	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAWC04 5'
7985	17835	28075	17.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7985	17835	28076	17.08	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
9193	18928		2.05	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
9513	19126		1.51	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
9859	19350		1.67	1.0E+00	AB040950.1	NT	Homo sapiens mRNA for KIAA1517 protein, partial cds
1553	11458	21315	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1553	11458	21316	0.84	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2598	12467	22360	0.9	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	13468		1.18	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5461	15381	25441	9.22	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
7336	17204		1.38	9.9E-01	U65667.1	NT	Lycopersicon esculentum putative Mi1 copy 1 nematode-resistance gene
7510	17298		2.43	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
8097	17988	28237	2.92	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
512	10454	20265	2.32	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13644	23429	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3732	13644	23430	0.82	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
6272	16137	26292	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6272	16137	26293	4.61	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
8362	18239	28487	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8362	18239	28488	4.43	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
9408	19061		1.62	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
5106	14974		1.01	9.7E-01	AI660384.1	EST_HUMAN	we62e04.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2345694 3'
6248	16114	26266	2.37	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
6952	16830	27023	1.86	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
6954	16832	27025	1.74	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
8510	18382		4.52	9.7E-01	BF511209.1	EST_HUMAN	UI-H-BI4-aol-e-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
9956	19419		1.39	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4337	14234	24016	6.8	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	14251	24036	1.3	9.6E-01	AW799674.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5083	14953	24729	0.92	9.6E-01	7662375	NT	Homo sapiens KIAA0914 gene product (KIAA0914), mRNA
5517	15435	25498	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
5517	15435	25499	3.46	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2994
6890	16769		1.37	9.6E-01	X95275:1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
8808	18622	28912	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
8808	18622	28913	4.15	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
9709	19646	24989	1.52	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3715	13627	23410	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3715	13627	23411	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
7266	17143	27336	1.17	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-b02 CT0295 Homo sapiens cDNA
3165	13090		3.37	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3181	13106		1.67	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9354	19029		1.64	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3869929 5'
9708	19564		1.43	9.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1700	11601		1.11	9.3E-01	AF242382.1	NT	Homo sapiens phytanoyl-CoA hydroxylase (PHYH) gene, exon 5

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2594	12464	22357	1.13	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
3949	13857	23630	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	13857	23631	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5155	15022		1.54	9.3E-01	AF075615.1	NT	Equus caballus microsatellite LEX013
5434	15354	25410	1.62	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5482	15402	25465	3.84	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
6701	16581	26771	1.88	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
9822	19325		1.56	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds
9954	19418		1.38	9.3E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Li>
3201	13125	22930	3.04	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5643	15556	25649	4.23	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
7618	17469	27688	1.38	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
7890	17740	27983	3.63	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
7952	17802	28041	1.73	9.2E-01	BF593251.1	EST_HUMAN	7o58e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 ;
8960	18767	29059	1.85	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
9006	18809	29101	2.01	9.2E-01	BF680047.1	EST_HUMAN	602154769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295896 5'
2077	11967		1.43	9.1E-01	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3169	13094	22898	0.97	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3169	13094	22899	0.97	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
4310	14207	23991	0.86	9.1E-01	U68172.1	NT	Rattus norvegicus mucin (MUC2) gene, partial cds
5919	15824	25950	2.92	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6472	16331	26498	15.99	9.1E-01	AA806623.1	EST_HUMAN	ob71g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
6551	16409	26587	2.2	9.1E-01	U72995.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
9445	19641		30.05	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3170	13095	22900	0.89	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4282	14181	23959	2.37	9.0E-01	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
4946	14822	24589	0.82	9.0E-01	AF017729.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
6388	16250		1.45	9.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5494	15413	25476	2.08	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5786	15692		1.32	8.9E-01	X60986.1	NT	Rabbit MHC fragment RLA-DF DNA
8990	18794	29085	3.47	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
9285	18987		4.74	8.9E-01	AE002186.2	NT	Chlamydophila pneumoniae AR39, section 21 of 94 of the complete genome
4442	14336	24126	3.28	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
8430	18304	28560	2.98	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
9108	19722		1.75	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
457	10401	20218	1.54	8.7E-01	AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2353	12233	22130	1.09	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2845	12773	22560	4.64	8.7E-01	AA595863.1	EST_HUMAN	nn05f11.s1 NCI_CGAP_Pr4.1 Homo sapiens cDNA clone IMAGE:1076877
4938	14816		2.51	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put>
7613	17464	27681	1.45	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
8206	18090	28343	5.47	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
8970	18776	29067	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
8970	18776	29068	4.16	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
9488	19534		2.78	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGYG07 3'
466	10409		1.66	8.6E-01	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
840	10767	20618	3.62	8.6E-01	W69089.1	EST_HUMAN	zd44e03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2224	12109	22012	1.01	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3568	13482	23273	0.81	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3730	13642	23427	1.29	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
5595	15509	25586	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5595	15509	25587	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6030	15934	26065	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6030	15934	26066	2.14	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6626	16506		1.52	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
6443	16304	26469	2.75	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7924	17774	28013	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds
7924	17774	28014	1.36	8.5E-01	AB006799.1	NT	Cyanidium caldarium gene for SigC, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9430	19643		2.52	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA
9436	19076		2.63	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
9683	19238	25243	1.29	8.5E-01	AB030818.1	NT	Mus musculus mper1 gene for period1, complete cds
4108	14008	23785	0.84	8.4E-01	AF143509.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5378	19443	25145	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5378	19443	25146	2.7	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571		3.13	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
724	10656	20486	2.31	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3056	12983	22774	2.64	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3739	13651	23434	1	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3930	13839	23619	3.11	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4917	14796	24570	1.12	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
4917	14796	24571	1.12	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14796	24570	0.95	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5177	14786	24571	0.95	8.3E-01	U46916.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB2
5222	15145	24839	2.13	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7573	17424		4.2	8.3E-01	AI791952.1	EST_HUMAN	nn01f12.y5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.t1 THR repetitive element ;
7822	17672	27914	1.23	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
7867	17717	27962	3.1	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
8062	17953	28204	2.46	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
8076	17967		2.46	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
8623	18488	28760	2.03	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2006	11898	21789	2.99	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2043	11934		1.51	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2646	12513		1.14	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-161199-031-C08 CT0219 Homo sapiens cDNA
5045	14917	24691	1	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6122	16016	26154	3.26	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
6309	19462	26330	3.58	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7788	17638	27871	1.53	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
7937	17787	28028	6.66	8.2E-01	Q9JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7937	17787	28029	6.66	8.2E-01	Q9JI70	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8909	18717	29011	2.81	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8966	18772	29064	6	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8971	18777	29069	6.65	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
9451	19083	25284	1.73	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2731	12593		1.29	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3412	13329	23130	2.81	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
3412	13329	23131	2.81	8.1E-01	AF055066.1	NT	Homo sapiens MHC class 1 region
5992	15897	26020	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
5992	15897	26021	2.49	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8775	18592	28879	1.94	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8775	18592	28880	1.94	8.1E-01	BE938558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
9166	18909	25343	1.84	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
170	10142		3.02	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pta gene for phosphate actyltransferase allele 15
285	10250	20070	3.76	8.0E-01	AJ132772.1	NT	Bos taurus futb and rlf genes
1990	11884		1.83	8.0E-01	BF530962.1	EST_HUMAN	602072473F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3039	12967	22761	2.73	8.0E-01	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3273	13194	22993	1.14	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3643	13557		1.8	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4432	14327	24116	5.65	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
6661	16541		2.84	8.0E-01	AW901489.1	EST_HUMAN	RC0-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
446	10390	20211	3.78	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
698	10631		1.16	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1587	11491		65.97	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1462 protein, partial cds
1634	11538		1.37	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2216	12102	22006	5.24	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2217	12103	22007	2.29	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3472	13388	23193	2.75	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4204	14103		0.92	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535786 5'
4508	14401	24188	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4508	14401	24189	1.02	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5075	14945	24720	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5075	14945	24721	0.84	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5084	14954		1.01	7.9E-01	M29930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6721	16601	26790	2.43	7.9E-01	X90996.1	NT	P.sativum GR gene
7504	17373	27582	4.78	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
7781	17631	27864	3.95	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249		2.36	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8543	18415	28682	2.48	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
858	10784		1.75	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2229	12114	22016	3.2	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4603	14491	24278	0.79	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5698	15607	25709	2.32	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
7323	17199	27399	1.27	7.8E-01	Y10159.1	NT	D.discoideum racGAP gene
9424	19623		1.42	7.8E-01	L29260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
138	10112	19932	6.33	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	10641		1.85	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha *chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;* butyrophilin-like (NG9), butyrophilin-li>
2680	12545	22436	2.8	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE
3313	13234		0.8	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNAC-T7), mRNA
3549	13464	23259	4.45	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4297	14195	23979	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4297	14195	23980	2.88	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5415	15335	25386	1.44	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5415	15335	25387	1.44	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5626	15541	25630	1.95	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9212	10112	19932	2.6	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	19004		6.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5710	15618	25720	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5710	15618	25721	4.04	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6699	16579	26770	1.41	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; tPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
6726	16606	26796	2.04	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
6726	16606	26797	2.04	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
7184	17061	27252	1.28	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbitol inducible, type a (Cyp2b9), mRNA
7347	17215	27414	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27415	7.52	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
8664	18553	28837	2.31	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
8664	18553	28838	2.31	7.6E-01	X86347.1	NT	H.aspersa mRNA for neurofilament NF70
8948	18756		4.81	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18850		2.74	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
502	10444		1.52	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
569	10508	20315	2.23	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3316	13236	23040	0.88	7.5E-01	C14203.1	EST_HUMAN	C14203 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-037E11 5'
4573	10083	19900	13.92	7.5E-01	8922672	NT	Homo sapiens hypothetical protein FLJ10793 (FLJ10793), mRNA
9381	19042		3.57	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
9828	19329	25209	1.87	7.5E-01	D90907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885
9884	19368	25190	1.42	7.5E-01	AE000823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1114	11029	20869	1.23	7.4E-01	AI598146.1	EST_HUMAN	tn14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element;contains element MIR repetitive element ;
2295	12177	22076	0.97	7.4E-01	AB011106.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3665	13579	23366	1.22	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4213	14111	23889	4.43	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7258	17135	27328	7.23	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
8041	18828		3.28	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1nh), mRNA
9150	18901		1.59	7.4E-01	AI472641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4515	14408	24194	0.95	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4602	14490	24277	4.76	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5127	14994		1.1	7.3E-01	5360211	NT	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5984	15889	26010	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
5984	15889	26011	5.61	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene

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Single Exon Probes Expressed in Heart

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6454	16315	26480	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
6454	16315	26481	7.42	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
8729	18585	28870	3.29	7.3E-01	AA678019.1	EST_HUMAN	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
8729	18585	28871	3.29	7.3E-01	AA678019.1	EST_HUMAN	zi25b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
814	10742		2.54	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
1914	11809	21687	3.68	7.2E-01	X79140.1	NT	N.tabacum NeIF-4A13 mRNA
2412	12289	22186	1.46	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3028	12956	22748	1.16	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3406	13323	23124	2.14	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-I allele, complete cds
3795	13707	23494	1.31	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4660	14546	24335	2.41	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5064	14934	24706	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
5064	14934	24707	1.16	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
6923	16801	26994	1.21	7.2E-01	AF236061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
7922	17772	28011	2.22	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
8121	18009	28256	4.78	7.2E-01	U82623.1	NT	Rattus norvegicus cytocentrin mRNA, complete cds
9570	19160		4.08	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
677	10610	20431	10.38	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3024	12952	22745	10.8	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4114	14014	23793	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4114	14014	23794	2.93	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
5623	15538	25625	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
5623	15538	25626	1.56	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296344 5'
6149	16022	26162	6.97	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyltetrahydropterin synthase (pr) gene, complete cds
7669	17519	27746	2.25	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
9363	19550		1.61	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'
1209	11118	20966	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209	11118	20967	1.04	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2399	12277	22173	1.4	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2399	12277	22174	1.4	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4989	14864		1.95	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6880	16759		8.1	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
8463	18336	28599	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
8463	18336	28600	2	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04 5'
954	10878	20725	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10878	20726	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1288	11196	21049	2.21	6.9E-01	AA593530.1	EST_HUMAN	nn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3182	13107	22911	1.63	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3399	13316	23117	0.85	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
6652	16532	26726	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6652	16532	26727	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8582	18450	28719	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
8582	18450	28720	3.56	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
9016	19543		2.37	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14)
941	10866	20713	1.03	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2639	12506		1.16	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2799	11502	21362	1.58	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_rna1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4469	14363	24153	1.26	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon III and flanks
4749	14634	24420	0.83	6.8E-01	4758521	NT	Homo sapiens hevin (HEVIN) mRNA
7556	17407	27622	1.52	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
8437	18311	28566	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
8437	18311	28567	2.34	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
8458	18331	28593	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8458	18331	28594	2.59	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8619	18485	28757	1.79	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
295	10259	20080	29.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
336	10295	20110	19.53	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA451664.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2120	12713	21908	3.59	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmo) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2966	12893	22692	3.7	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4350	14246	24032	0.96	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	14762	24538	0.85	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2574598 3'
5182	15046	24811	0.89	6.7E-01	AJ252942.1	NT	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial
5627	15542	25631	1.62	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
5817	15723	25836	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
5817	15723	25837	1.42	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6329	16192		3.98	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
6342	16205	26367	1.46	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8323	18200	28449	2.23	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
8754	17903	28147	3.69	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI1
2462	12329	22227	0.87	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIL2) mRNA, partial cds
2667	12532	22422	1.29	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13362	23168	1.04	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3608	13522	23310	3.05	6.6E-01	Y07669.1	NT	C.albicans random DNA marker, 282bp
4020	13924		0.87	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5822	15728	25840	3.96	6.6E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6525	16384	26563	3.63	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
7571	17422		2.41	6.6E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9619	19197	25256	1.35	6.6E-01	AE004382.1	NT	Vibrio cholerae chromosome II, section 39 of 93 of the complete chromosome
608	10544	20352	1.37	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	10544	20353	1.37	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3386	13304	23104	5.1	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
3951	13859	23633	1.08	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4185	14085	23860	4.17	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4215	14113	23890	0.86	6.5E-01	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
4994	14869	24632	2.27	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5175	15041		0.88	6.5E-01	U37258.1	NT	Acetobacter xylinum putative ATP binding protein delta-AceB gene, partial cds, and GDP-mannose:cellobiosyl-diphosphopolyprenol alpha-mannosyltransferse gene, complete cds
6036	15939	26071	1.38	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7919	17769	28008	2	6.5E-01	AF119676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
8030	17922	28168	3.24	6.5E-01	H87583.1	EST_HUMAN	yw17f06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252515 5'
8073	17964	28215	4.03	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
8170	18058		4.27	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
8877	18689	28981	2.3	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
9419	19069		2.79	6.5E-01	BE465050.1	EST_HUMAN	hv74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
9651	19490		1.69	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
252	10218	20035	5.4	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3410	13327	23128	2.46	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3785	13697	23484	1.34	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4389	14285	24066	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
4389	14285	24067	0.84	6.4E-01	Y12488.1	NT	M.musculus whn gene
7007	16884	27076	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
7807	17657	27895	13.62	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
7818	17668	27908	1.44	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
9528	19135		6.34	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'
9951	19553		1.65	6.4E-01	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
427	10372	20196	4.41	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
524	10466	20277	2.15	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2116	12005	21903	3.87	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2534	12408	22300	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2534	12408	22301	3.89	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12911		0.93	6.3E-01	Y17275.1	NT	Lycopersicon esculentum p69a gene, complete CDS

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3985	13892	23668	1.38	6.3E-01	X99675.1	NT	D.melanogaster mRNA for metabotropic glutamate receptor
6959	16837		3.17	6.3E-01	BE902044.1	EST_HUMAN	601676889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
7150	17027	27223	1.67	6.3E-01	S62927.1	NT	glycoprotein IIIa {Alu 1 and 3 fusion junction} [human, Genomic Mutant, 300 nt]
7421	17288	27495	2.72	6.3E-01	9627521	NT	Variola virus, complete genome
7421	17288	27496	2.72	6.3E-01	9627521	NT	Variola virus, complete genome
8004	17854	28095	1.4	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
8413	18288	28543	2.27	6.3E-01	AA877715.1	EST_HUMAN	nr09h06.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:O02916 O02916 HLARK. ;
8647	18511	28791	11.72	6.3E-01	AI904160.1	EST_HUMAN	CM-BT043-090299-046 BT043 Homo sapiens cDNA
8725	18581	28865	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
8868	18680	28969	1.98	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
9128	19697	24899	9.21	6.3E-01	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9220	18944		1.54	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
9435	19619		1.58	6.3E-01	X83528.1	NT	C.limicola pscD gene
5578	15493	25569	2.12	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
6426	16287		3.06	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
6831	16710	26903	5.45	6.2E-01	H72255.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
7435	16448	26638	1.71	6.2E-01	BE562687:1	EST_HUMAN	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
7476	17336		2.56	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
7799	17649	27886	7.14	6.2E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
8007	17857	28100	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2345	12225		4.5	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4931	14809	24577	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
4931	14809	24578	0.99	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
6104	15998	26134	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6104	15998	26135	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6792	16671	26863	3.72	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
7108	16985	27175	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
7108	16985	27176	1.75	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 4 (MAP4K4), mRNA
7419	17286	27492	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
7419	17286	27493	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

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7778	17628	27860	1.59	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
486	10429	20243	0.92	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10490		2.64	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1339	11245	21103	1.76	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3744	13656	23438	1.02	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
5227	15151	24918	1.56	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5339	15260	25086	2.58	6.0E-01	AW139713.1	EST_HUMAN	UI-H-BI1-aeb-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
5940	15845	25968	2.61	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6350	16213	26375	6.2	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6725	16605	26794	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6725	16605	26795	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7653	17503	27727	1.69	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
7894	17744		1.43	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
8411	18286	28541	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8411	18286	28542	1.78	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
8838	18651	28939	2.74	6.0E-01	AI420623.1	EST_HUMAN	tf08f07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095621 3'
9500	19115	25291	1.64	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
9787	19554	25065	2.1	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9809	19484		2.18	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
984	10907	20752	1.25	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	13156	22954	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3232	13156	22955	4.85	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4129	14029		4.12	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
5889	15795	25917	2.1	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8061	17952	28203	2.67	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8328	18205	28454	3.1	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
8529	18401	28669	2.36	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/Ei CD48 antigen (Cd48) gene, partial cds
9165	18908	25342	1.91	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
9404	19057		2.18	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
9614	19193		4.15	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1867	11763	21637	1.44	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3902	13812	23596	0.96	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4413	14307	24090	2.81	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4690	14576		1.04	5.8E-01	AF110846.1	NT	Megaselia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5753	15661	25768	1.29	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6077	16060		2.3	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6604	16484		2.62	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
6764	16643	26830	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6764	16643	26831	2.23	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
7153	17030	27224	8.64	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8358	18235	28483	8.47	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8396	18272		3.23	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
8482	18355		1.78	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3186	13111	22916	1.48	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
3460	13376		2.43	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3829	13741	23533	1.65	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S7*2-BJ1S1) mRNA, partial cds
5201	15064	24827	2.24	5.7E-01	U78517.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
5836	15742	25854	3.72	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6100	15110	24874	1.41	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6564	16422	26603	2.12	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
9124	18883		1.68	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-a02 HT0736 Homo sapiens cDNA
3318	13239	23043	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	13239	23044	1.21	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3808	13720	23509	0.83	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4146	14046	23818	0.83	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
7111	16988	27180	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
7111	16988	27181	4.16	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCFSF05 5'
9023	18817		2.46	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
9137	18893	28794	1.73	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element ;
9524	19133		1.32	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9919	19392		3.09	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1193	11103	20949	1.09	5.5E-01	8393912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2668	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2668	12533	22424	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2888	12815	22608	1.34	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3027	12955		1.39	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3196	13121	22926	3.1	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	13548	23335	1.29	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	10113	19933	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	10113	19934	3.74	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	10509	20316	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
570	10509	20317	2.61	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
1250	11157	21006	2.24	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2059	11949		2.78	5.4E-01	AE002247.2	NT	Chlamydophila pneumoniae AR39, section 74 of 94 of the complete genome
2208	12095	21998	2.23	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
7738	17588		2.01	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
8427	18301	28557	2.87	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8892	18702	28996	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8892	18702	28997	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
9087	18862		2.12	5.4E-01	AI858398.1	EST_HUMAN	wl37g04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
505	10447	20260	2.02	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
2093	11982	21877	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	11982	21878	0.91	5.3E-01	AF113919.1	NT	Brassica oleracea var. capitata phospholipase D2 (PLD2) gene, complete cds
2755	12617	22508	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	12617	22509	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3205	13129	22931	2.92	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4117	14017		1.29	5.3E-01	U39687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5350	15270	25098	1.75	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5350	15270	25099	1.75	5.3E-01	AI820921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5467	15387	25447	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5467	15387	25448	1.91	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
7161	17038		2.15	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
8846	18658	28946	5.62	5.3E-01	BE566291.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
9015	19551		2.46	5.3E-01	AA916053.1	EST_HUMAN	og30e05.s1 NCI_CGAP_Br7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611 APOLIPOPROTEIN D PRECURSOR (HUMAN);
799	10728	20568	11.31	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1148	11061	20904	7.69	5.2E-01	Q9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1174	11086	20930	2.83	5.2E-01	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
1843	11739		5.04	5.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2099	11988	21886	2.75	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3081	13008	22798	1.9	5.2E-01	U65942.1	NT	Chlamydophila abortus strain S26/3 POMP91A and POMP90A precursor, genes, complete cds
3199	13124		1.22	5.2E-01	D73443.1	NT	Azotobacter vinelandii icd gene for isocitrate dehydrogenase, complete cds
3359	13278		1.76	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3397	13314	23114	1.9	5.2E-01	AA984165.1	EST_HUMAN	am77g05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3580	13494		1.13	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3582	13496	23287	1.06	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Ll>
4949	14826		1.29	5.2E-01	7106444	NT	Mus musculus vanilloid receptor-like protein 1 (Vrl1), mRNA
7761	17611	27837	1.28	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
9719	19260	25221	2.46	5.2E-01	AW137066.1	EST_HUMAN	UI-H-BI1-acp-a-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714799 3'
9887	19370		3.43	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
601	10537	20347	1.89	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
632	10569	20381	3.28	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
632	10569	20382	3.28	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain Pl vt1) 16S rRNA gene
1632	11536		1.06	5.1E-01	X87885.1	NT	*R.norvegicus mRNA for mammalian fusca protein*
1977	11870		1.44	5.1E-01	BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
3984	13891	23667	3.84	5.1E-01	AI858495.1	EST_HUMAN	wl39b12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427263 3'
4094	13994	23771	2.86	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
6133	15980	26116	1.57	5.1E-01	R80873.1	EST_HUMAN	yi94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
7584	17435	27650	4.54	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
7586	17437	27653	3.57	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9230	19478		3.62	5.1E-01	BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
9473	19100		2.03	5.1E-01	BF439982.1	EST_HUMAN	nac51f10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element *TAR1 repetitive element ;*
2087	11977	21871	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2087	11977	21872	1.37	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2097	11986	21882	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2097	11986	21883	1.32	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3688	13601	23388	0.84	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3797	13709	23495	3.44	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6961	16839		5.62	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
7442	16455	26644	3.61	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
7550	17401	27614	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7550	17401	27615	2.25	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
7941	17791		1.27	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
9003	18806	29099	9.32	5.0E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
9170	18913		2.26	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
9858	19349		2.02	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
9869	19358		2.94	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.98	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1864	11760	21634	1.39	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5679	15588	25688	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15588	25689	2.46	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6406	16267	26429	1.76	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	BF209791.1	EST_HUMAN	601874964F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
7359	19768		2.2	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
9065	18846		1.43	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9851	19733		3.55	4.9E-01	AA613562.1	EST_HUMAN	nq22e11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
4577	14136		1.12	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5381	15300	25153	8.94	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6018	15922		3.94	4.8E-01	AA659878.1	EST_HUMAN	nu85f09.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
6330	16193		1.96	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
6563	16421	26601	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26602	3.82	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6613	16493	26679	1.16	4.8E-01	AI820744.1	EST_HUMAN	yj77f10.y5 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element ;
8111	18001		2.04	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
9369	19511		2.52	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
9870	19359		2.26	4.8E-01	BE790632.1	EST_HUMAN	601584324F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938909 5'
5925	15830	25953	8.36	4.7E-01	BF217173.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
8221	18103		5.77	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
8434	18308	28564	2.06	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
8682	18570	28853	2.43	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
9390	19049		1.36	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909198 3'
3674	13588	23375	1.27	4.6E-01	AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA
3683	13597	23383	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	13597	23384	1.28	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		0.97	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5360	15280	25111	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15280	25112	3.38	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5414	15334	25384	3.29	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN. ;
5414	15334	25385	3.29	4.6E-01	AI247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN. ;
5418	15339	25393	1.58	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6057	16040	26181	1.47	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057	16040	26182	1.47	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6843	16722	26916	13.48	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7363	17230	27430	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7363	17230	27431	26.48	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730	17580	27802	1.33	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7730	17580	27803	1.33	4.6E-01	AI915634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
8359	18236		2.86	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
8368	18245	28495	4.78	4.6E-01	BE185449:1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8368	18245	28496	4.78	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
8766	17915	28160	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8766	17915	28161	5.45	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
9313	19005		1.43	4.6E-01	D53316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-105F03 5'
9978	19491		2.21	4.6E-01	AF120134.1	NT	Linanthus jamauensis maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
1869	11765	21639	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1869	11765	21640	1.73	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2841	12769	22558	4.87	4.5E-01	AA677086.1	EST_HUMAN	zj55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3275	13196	22996	3.97	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3331	13251	23056	1.05	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3942	13850		1.41	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
3982	13889	23665	1.1	4.6E-01	AI708908.1	EST_HUMAN	as96e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4085	15079		4.02	4.5E-01	AW873495.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.5E-01	BE963445.2	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5406	15325	25375	1.45	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
5983	15888		1.47	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	AI858849.1	EST_HUMAN	wi32e02.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923 SWI/SNF COMPLEX 170 KDA SUBUNIT. ;
6897	16776	26970	3.14	4.5E-01	AI648596.1	EST_HUMAN	tz56g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
7100	16977		1.54	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
7991	17841	28082	25.09	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
7991	17841	28083	25.09	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY17
8237	18117	28369	2.42	4.5E-01	AW591271.1	EST_HUMAN	xo14h01.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1] ;
9036	19724		2.25	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
9694	19245		1.44	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
9763	19283		2.15	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
9974	19652	24987	1.83	4.5E-01	AF238234.2	NT	Entamoeba histolytica diaphanous protein (dia) gene, partial cds
1991	11885		2.47	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Itmap1), mRNA
2340	12220	22118	3.59	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	13195	22994	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3274	13195	22995	0.99	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3277	13198	22998	1.87	4.4E-01	BF056726.1	EST_HUMAN	7j91d02.y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4141	14041		1.33	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
4924	14803		0.93	4.4E-01	BE141396.1	EST_HUMAN	MR0-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5326	15246	25050	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	15246	25051	1.99	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5490	15409	25474	1.3	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5499	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
5624	15539	25627	1.6	4.4E-01	AI198413.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
5624	15539	25628	1.6	4.4E-01	AI198413.1	EST_HUMAN	qi62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN ;
5782	15688	25798	1.79	4.4E-01	AW080795.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE. ;
6582	16462		10.84	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced stolon tip protein (partial)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422	1.29	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
7723	17573	27798	1.99	4.4E-01	AI268650.1	EST_HUMAN	qo39f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
7724	17574		2.45	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
7813	17663	27903	4.67	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
7935	17785	28025	1.33	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
7935	17785	28026	1.33	4.4E-01	S76404.1	NT	beta -HKA=H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
9296	18996	25329	2.29	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
9306	19663		3.29	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9731	19267	25224	5.34	4.4E-01	9627742	NT	Autographa californica nucleopolyhedrovirus, complete genome
9824	19326		1.76	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
405	10351	20178	1.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
405	10351	20179	1.98	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
1585	11489	21350	1.1	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2843	12771		0.96	4.3E-01	AW935269.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3022	12950	22742	0.93	4.3E-01	AW999477.1	EST_HUMAN	MR0-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
3221	13145		1.53	4.3E-01	AE000698.1	NT	Aquifex aeolicus section 30 of 109 of the complete genome
4059	13961	23737	1.15	4.3E-01	J00306.1	NT	Human somatostatin I gene and flanks
4306	10351	20178	1.02	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4306	10351	20179	1.02	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4875	14755		1.11	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No: 14
5059	14929		1.06	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5600	15514	25592	3.04	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSC186) gene, partial cds
6029	15933	26064	3.86	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifnG gene
6102	15996		4.01	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
6393	16255		2.54	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158296 5'
6909	16787		2.83	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-I (flaC-flaI) genes, complete cds
7608	17459	27674	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
7608	17459	27675	1.65	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
7872	17722	27967	1.27	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2. ;
8302	16049	26195	2.64	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
8537	18409	28673	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
8537	18409	28674	1.98	4.3E-01	AW993658.1	EST_HUMAN	RC3-BN0034-290200-013-c12 BN0034 Homo sapiens cDNA
9916	19390		2.02	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1335	12691	21099	1.04	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11800		0.89	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3558	13472	23263	4.78	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3585	13499	23288	1.09	4.2E-01	AI280338.1	EST_HUMAN	ql94b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3803	13715	23503	0.96	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-h01 LT0015 Homo sapiens cDNA
3900	13810	23595	1	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4545	14438		3.63	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4599	14487	24273	4.96	4.2E-01	AA534093.1	EST_HUMAN	nj69h01.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25484	1.5	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5533	15450	25518	1.56	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6151	16024	26165	9.1	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
6184	19461	26219	2.1	4.2E-01	S82504.1	NT	Brca1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
6217	16083	26233	5.91	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6663	16543	26739	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6663	16543	26740	2.1	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
6776	16655	26844	1.19	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7992	17842	28084	1.48	4.2E-01	AW863666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
8400	18276	28528	2.2	4.2E-01	AB023489.1	NT	Oryzias latipes OlGC7 mRNA for membrane guanylyl cyclase, complete cds
8699	18517	28799	2.04	4.2E-01	BE966485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
9863	19353		1.66	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'
1078	10994	20835	1.88	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1087	11003	20844	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1087	11003	20845	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1592	11496	21356	1.03	4.1E-01	AI905949.1	EST_HUMAN	PM-BT103-270499-684 BT103 Homo sapiens cDNA
2678	12543	22434	1.52	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	12836	22633	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12836	22634	1.76	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	13186	22985	1.13	4.1E-01	AA906344.1	EST_HUMAN	oj94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
4177	14077	23852	2.59	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 IsoG, IsoH, IsoI, IsoJ, IsoA, IsoB, IsoC, IsoD, IsoE and IsoF genes
4208	14107		1.07	4.1E-01	AA909257.1	EST_HUMAN	om33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4373	14269		0.83	4.1E-01	R41726.1	EST_HUMAN	yg11b03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31814 3'
4567	14459	24247	1.26	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5185	15049		0.87	4.1E-01	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
5644	15557	25650	4.13	4.1E-01	BF681393.1	EST_HUMAN	602166590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6395	16257	26418	2.91	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
6683	16563	26757	1.3	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
7253	17130	27323	1.23	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitpec-pending), mRNA
7888	17738		1.3	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
8018	17868		1.58	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-e08 HT0137 Homo sapiens cDNA
8213	18097	28349	164	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
8696	17880	28121	2.79	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HBK1)
9624	19702		1.72	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1023	10940	20783	1.27	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1316	11223	21079	0.96	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1469	11374		4.06	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1960	12709	21742	1.17	4.0E-01	Z96933.1	NT	Ascobolus immersus masc2 gene
1960	12709	21743	1.17	4.0E-01	Z96933.1	NT	Ascobolus immersus masc2 gene
2774	10110	19931	1.09	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 componen n-recognin (Ubr1), mRNA
2939	12866	22665	2.24	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2939	12866	22666	2.24	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3637	13551	23339	1.61	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae YllC (ylIC), YllD (ylID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3755	13668	23451	3.24	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3755	13668	23452	3.24	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4712	14598		7.34	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5603	15517	25596	1.31	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
8959	18766		3.24	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
9312	19567		2.22	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9825	19327		1.33	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
9910	19387		1.4	4.0E-01	AL139075.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 2/6
227	10196	20007	1.59	3.9E-01	AW352188.1	EST_HUMAN	CM4-HT0136-150999-014-f09 HT0136 Homo sapiens cDNA
1356	11262	21119	2.1	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2605	12473	22367	3.54	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2673	12538	22427	5.98	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
2673	12538	22428	5.98	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3058	12985	22776	3.63	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egl, syrB2, cya3 genes and orf3
3988	13895	23672	1.47	3.9E-01	BF592611.1	EST_HUMAN	7i61d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
4919	14798	24572	1.48	3.9E-01	BE728667.1	EST_HUMAN	601563948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
5613	15528	25611	3.53	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
7324	17200	27400	1.5	3.9E-01	AW195888.1	EST_HUMAN	xn86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN ;
7503	17372	27581	1.4	3.9E-01	AI937337.1	EST_HUMAN	wp76a02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
7680	17530	27755	2.97	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
8195	18080		2.22	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBQC11 5'
9091	19642		2.49	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9209	18940		2.38	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
9288	18990	25328	1.26	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
154	10128		7.44	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1827	11724		1.22	3.8E-01	AE003870.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2524	12398	22289	2.44	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds
2591	12726	22352	4.41	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2972	12899		0.92	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3010	12938	22732	2	3.8E-01	AF043383.1	NT	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
3438	13355	23160	7.77	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3494	13410		0.79	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3506	13410		0.91	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3841	13752	23545	0.85	3.8E-01	6754095	NT	Mus musculus general transcription factor II I (Gtf2i), mRNA
5046	14918	24692	0.98	3.8E-01	BE544653.1	EST_HUMAN	601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
5445	15366	25422	1.62	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
5994	15899	26023	4.47	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-049-e02 BT0537 Homo sapiens cDNA
6053	16036	26177	3.81	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
6438	16299		4.83	3.8E-01	X61597.1	NT	M.musculus gene for kallikrein-binding protein
6980	16857	27052	3.07	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7516	17304		4.11	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element;contains PTR5 repetitive element ;
8820	18633		2.82	3.8E-01	BE719219.1	EST_HUMAN	RC0-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
8939	18747	29041	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
8939	18747	29042	2.57	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
9297	18997		2.38	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
9422	19661		1.34	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
9530	19137		2.21	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
9917	19638		1.84	3.8E-01	AF291483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1ra4) gene, complete cds
9921	19675	24993	1.37	3.8E-01	T54787.1	EST_HUMAN	yb42b11.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar to gb:A06977 SERUM ALBUMIN PRECURSOR (HUMAN)
9937	19406	25180	1.3	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
9970	19430	25151	1.33	3.8E-01	AA776820.1	EST_HUMAN	ah37b01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1291657 3' similar to TR:Q15288 Q15288 NO DISTINCTIVE PROTEIN MOTIFS. ;
2431	12308	22203	9.85	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3414	13331	23133	9.48	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4136	14036	23812	6.63	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4225	14123	23898	1.53	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4292	14190	23974	3.32	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6235	16101	26250	2.73	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6392	16254	26415	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6392	16254	26416	4.51	3.7E-01	BE873743.1	EST_HUMAN	601483887F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886652 5'
6848	16727	26921	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
6848	16727	26922	2.34	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7307	17183		1.46	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCDO gene)
7864	17714	27958	3.93	3.7E-01	AI336411.1	EST_HUMAN	qt46b07.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
8232	18113	28365	1.81	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
8392	18268	28518	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8392	18268	28519	2.66	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
8762	17911	28155	4.23	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
8979	18784		2.76	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
9008	19303		1.87	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
9176	18917		1.94	3.7E-01	AJ243526.1	NT	Chlamydophila psittaci partial omp1 gene for outer membrane protein 1
9272	18976		2.41	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9634	19206		2.18	3.7E-01	AL121154.1	EST_HUMAN	DKFZp762K075_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K075 5'
9701	19251	25217	1.52	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9964	19746		1.31	3.7E-01	AJ237934.1	NT	Bos taurus partial stat5B gene, exons 2-15 and joined CDS
979	10902		7.17	3.6E-01	U89241.1	NT	Human mibp gene, partial cds
1292	11199	21054	2.59	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1292	11199	21055	2.59	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1874	11770	21645	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1874	11770	21646	6.05	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947419 3'
1908	11803	21682	6.18	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.08	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108		1.04	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	NT	P.irregulare (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2589	12460	22350	2.28	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2869	15077		8.9	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3424	13341	23145	1.85	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76758.1	NT	H.sapiens serotonin transporter gene, exons 9 and 10
4308	14205	23988	1.16	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4635	14523	24312	0.85	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4684	14570	24367	1.23	3.6E-01	AJ229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4941	14819	24587	2.01	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5899	15805	25928	1.6	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
6238	16104		5.49	3.6E-01	R94090.1	EST_HUMAN	yt74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
6317	16180	26340	1.66	3.6E-01	AW027174.1	EST_HUMAN	wt72c10.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117 O15117 FYN BINDING PROTEIN. [1] ;
6816	16695	26886	13.42	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17082	27269	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17082	27270	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7674	17524	27750	15.34	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
8453	18326	28586	3.69	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
8741	17890	28134	3.56	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
9044	19761		1.81	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
9127	18886		3.05	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
9281	18983		3.03	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704		1.58	3.6E-01	AW190229.1	EST_HUMAN	xl60e11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679116 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
202	10174	19990	2.18	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
662	10596	20414	0.97	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
708	10640	20466	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10640	20467	1.24	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
763	10694	20531	3.17	3.5E-01	BF129796.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1603	11508	21370	1.17	3.5E-01	BF310688.1	EST_HUMAN	601894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2563	12725	22327	1.85	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2672	12537		0.86	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	14065	23839	1.92	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
4379	14275	24056	1.29	3.5E-01	BE146585.1	EST_HUMAN	RC5-HT0218-181099-011-g02 HT0218 Homo sapiens cDNA
4790	14675	24462	0.84	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
4849	14730	24513	3.84	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
6199	15959		3.47	3.5E-01	X98505.1	NT	S.scrofa mRNA for CD31 protein (PECAM-1)
6704	16584		1.88	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.6E-01	4507610	NT	Homo sapiens tyrosine kinase non-receceptor 1 (TNK1), mRNA
7612	17463	27680	1.51	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
7688	17538	27764	5	3.5E-01	Z26825.1	NT	X.laevis gene for albumin including HP1 enhancer
8116	18005	28251	2.99	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
8386	18263	28513	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8386	18263	28514	2.34	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8951	18758	29052	3.34	3.5E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	18937		2.12	3.5E-01	X64565.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
9941	19616	24999	2.26	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
9941	19616	25000	2.25	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
691	10624		1.9	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
960	10883	20731	4.53	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, orf222 and partial inaA gene
1304	11211	21066	1.73	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2352	12232	22129	2.81	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2642	12509	22400	1.46	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12898	22697	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	12898	22698	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22846	5.41	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3488	13404	23209	3.48	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3722	13634		2.33	3.4E-01	BF449010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1 ;
3966	13872		1.16	3.4E-01	AA584196.1	EST_HUMAN	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4394	14290	24074	0.78	3.4E-01	AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4544	14437	24221	1.82	3.4E-01	BE069912.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4828	14710	24494	0.93	3.4E-01	BE463761.1	EST_HUMAN	hy17d09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3197585 3' similar to contains L1.t3 L1 repetitive element ;
4870	14750		3.57	3.4E-01	AI240973.1	EST_HUMAN	qj95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
4970	14845	24614	1.2	3.4E-01	X16544.1	NT	Sea urchin hsp70 gene II for heat shock protein 70
5487	15406	25469	2.85	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5551	15467		4.71	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:547221 3'
5654	15566		2.06	3.4E-01	L02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
5716	15623	25724	2.57	3.4E-01	AW204505.1	EST_HUMAN	UI-H-BI1-ael-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
5780	15687	25796	1.47	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6045	15948		1.52	3.4E-01	N95225.1	EST_HUMAN	zb53e12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6148	16021	26161	1.41	3.4E-01	AI468082.1	EST_HUMAN	tm63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
6943	16821		1.77	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
7139	17016	27209	1.62	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
7313	17189	27390	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7313	17189	27391	3.88	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
7433	16446	26635	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7433	16446	26636	4.17	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7690	17540	27766	2.22	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8380	18257		4.09	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
8407	18283	28536	2.2	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
8440	18314	28672	2.26	3.4E-01	AF045981.1	NT	Rutilus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28742	1.77	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8604	18471	28743	1.77	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
8790	18605	28895	1.8	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-gicerin/MUC18, complete cds
8814	18627	28916	4.03	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9020	18814		2.01	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
9130	18887		1.3	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
9229	19508		1.82	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
9347	19024		4.9	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
9378	19538		2.49	3.4E-01	BE218652.1	EST_HUMAN	hv42h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.t3 PTR5 repetitive element ;
9432	19639		2.13	3.4E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
9537	19140	25264	1.79	3.4E-01	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9829	19330		1.79	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
14	10000	19791	7.91	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
100	10000	19791	3.92	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
440	10384	20208	1.16	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
617	10554	20366	1.41	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1182	11093	20940	3.05	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21046	4.82	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1588	11492	21352	1.11	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dtgn5), mRNA
1704	11605		1.05	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2919	12846	22848	2	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
2982	12910		1.12	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3016	12944	22737	1.01	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3450	13367	23173	1.14	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3738	13650	23433	2.17	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3884	13795	23582	1.59	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3920	13829	23609	1.92	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4271	14170		2.74	3.3E-01	D31662.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4589	14477		1.48	3.3E-01	AI539114.1	EST_HUMAN	tp78b12.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
5263	15185	24960	2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5263	15185	24961	2.68	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5622	15537	25623	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5622	15537	25624	2.71	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6117	16011	26148	3.64	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
6117	16011	26149	3.64	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;
6575	16433	26616	1.5	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6981	16858	27053	19.46	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
7477	17337	27542	3.26	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
7507	17295	27504	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
7739	17589		2.07	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
8104	17994	28242	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8104	17994	28243	2.71	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
8389	18265		1.82	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
8561	18431	28700	12.76	3.3E-01	BE219351.1	EST_HUMAN	hv51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8652	18541	28825	3.94	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8956	18763		4.79	3.3E-01	AA806621.1	EST_HUMAN	ob71g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
8972	10000	19791	1.88	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5JI nodX gene
9119	18881	28789	1.63	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
9817	19323		6.05	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
449	10393		1.98	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	10634		2.05	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1146	11059	20902	18.99	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	11168	21019	1.04	3.2E-01	Z50202.1	NT	P.vulgaris arc5-1 gene
1368	11274	21130	6.25	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	11638	21506	1.22	3.2E-01	Z36041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1744	11645	21513	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1744	11645	21514	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MAGD Homo sapiens cDNA
1800	11698	21574	1.16	3.2E-01	AL111655.1	NT	*Botrytis cinerea strain* T4 cDNA library under conditions of nitrogen deprivation
2114	12003	21901	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2494	12368		2.9	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pknox1), mRNA
2677	12542	22433	1.55	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3556	13470		0.96	3.2E-01	D10872.1	NT	Humam h NAT allele 3-2 gene for arylamine N-acetyltransferase
3868	13779		0.97	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4295	14193	23977	1.35	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4397	14293	24077	1.33	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME I PRECURSOR
4632	14520		5.86	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4907	15081		1.18	3.2E-01	M32352.1	NT	Mouse renin (Ren-1-d) gene, complete cds
5133	15000	24771	0.98	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5223	15146	24913	2.82	3.2E-01	BE173964.1	EST_HUMAN	CM0-HT0569-060300-269-f10 HT0569 Homo sapiens cDNA
6752	16631	26819	1.42	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
6872	16751	26946	13.32	3.2E-01	X02508.1	NT	H.sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6875	16754	26951	14.29	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6929	16807		1.35	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
6986	16863	27056	1.5	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
7247	17124		2.19	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
7910	17760		3.26	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8058	17949	28199	2.7	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDZ21
9152	19662		3.28	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
9669	19228		2.97	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9801	19313		1.58	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
9855	19696	24898	1.57	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2636	12503	22397	3.73	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:M64241 QM PROTEIN (HUMAN);
2665	12655	22419	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2665	12655	22420	3.45	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	12756		1.01	3.1E-01	AW629036.1	EST_HUMAN	hi46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3136	13061		2.78	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3832	13744	23536	1.15	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5073	14943	24717	0.99	3.1E-01	AA576308.1	EST_HUMAN	nm61h05.s1 NCI_CGAP_Br3 Homo sapiens cDNA clone IMAGE:1072761 3'
5365	15285	25119	8.66	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5447	15368		45.03	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5527	15444	25510	1.94	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
5890	15796	25918	1.34	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6160	19438	24861	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7023	16900	27092	1.87	3.1E-01	R45318.1	EST_HUMAN	yg46f01.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35639 3'
7791	17641	27874	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7791	17641	27875	7.76	3.1E-01	BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17682	27926	1.96	3.1E-01	AI244001.1	EST_HUMAN	qj61e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
8211	18095	28348	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
8823	18636	28920	1.99	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
9279	18982		1.63	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
9315	19007		1.64	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
9457	19089		2.45	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9806	19318		3.11	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
66	12635	19866	1.58	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
254	10220	20037	11.12	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1204	11114	20960	1.89	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1491	11396	21256	6.26	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2089	11978	21873	0.86	3.0E-01	AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	13100		0.98	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyguluronate lyase, complete cds
3789	13701	23488	1.34	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4412	14306	24089	1.91	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5283	15205	24981	5.34	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5379	15298	25147	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5379	15298	25148	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5401	15320	25368	3.51	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6086	16031	26171	2.61	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6335	16198	26358	2.57	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
6429	16290	26451	1.35	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
6626	16505	26693	1.25	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
6877	16756		4.67	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clecsf9), mRNA
6937	16815	27007	1.27	3.0E-01	BE566083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
7944	17794	28034	1.89	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
8980	18785	29074	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8980	18785	29075	2.89	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
9564	19647		1.43	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9836	19690		2.76	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1978	11871	21762	1.6	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2201	12088	21989	0.99	2.9E-01	AF222718.1	NT	Chrysodidymus synuroideus mitochondrion, complete genome
3147	13072	22873	1.03	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	13137	22939	2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3213	13137	22940	2.29	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3821	13733	23522	1.28	2.9E-01	AI610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN);contains element L1 repetitive element ;
3994	13901		0.82	2.9E-01	AW002902.1	EST_HUMAN	wr02f10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4384	14280	24059	1.01	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4388	14284	24064	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4388	14284	24065	0.78	2.9E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	14615	24401	0.92	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5218	15141		1.49	2.9E-01	R37485.1	EST_HUMAN	yf77e12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28291 3'
5522	15440	25504	4.45	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5522	15440	25505	4.45	2.9E-01	X56098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5529	15446	25513	5.83	2.9E-01	6679682	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
5818	15724	25838	2.24	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6171	15128	24847	1.51	2.9E-01	AF142329.1	NT	Mus musculus Flilh protein (Flilh) gene, complete cds; and Liglh protein (Liglh) gene, partial cds
6218	16084	26234	2.52	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
6249	16115	26267	1.74	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
6619	16499	26686	1.76	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
6619	16499	26687	1.76	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8267	18147	28387	1.96	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
8502	18375	28639	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8502	18375	28640	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8864	18676	28965	1.77	2.9E-01	AA935373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.t2 LTR8 repetitive element ;
8866	18678	28967	4.54	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
9514	19127	25260	1.63	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Brn25.Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER29 repetitive element ;
9602	19184	25248	2.74	2.9E-01	AF092453.1	NT	Homo sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds
9644	19212		1.33	2.9E-01	BE788199.1	EST_HUMAN	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
9883	19367	25188	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
556	10497		1.84	2.8E-01	U67136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1067	10983	20828	2.47	2.8E-01	AF168050.1	NT	Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11163	21013	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1256	11163	21014	1.1	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1269	11176	21025	1.01	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1696	11598	21470	1.55	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
1966	11860	21750	1.77	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586I2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586I2321
2084	11974	21869	1.47	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2423	12300	22197	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198	2.94	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2630	12498	22388	1.37	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2940	12867		1.49	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	12868	22667	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	12868	22668	2.48	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3332	13252	23057	1.1	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
3915	13824	23604	1.75	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	14003		2.21	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
4352	14248	24034	0.98	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038	2.2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14559	24352	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14559	24353	1.03	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14608	24394	2.8	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4755	14640	24427	1.54	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
4787	14672	24459	1.7	2.8E-01	AI272669.1	EST_HUMAN	ql59c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element;contains element LTR5 repetitive element ;
5252	19440	24948	21.36	2.8E-01	AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5443	15363	25419	2.33	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	15677	25784	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
5770	15677	25785	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6038	15941	26073	7.67	2.8E-01	BF511215.1	EST_HUMAN	UI-H-BI4-aci-f-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6713	16593	26781	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6713	16593	26782	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6778	16657	26847	2.39	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6994	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	602022987F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
7311	17187	27388	1.35	2.8E-01	AF080592.1	NT	Mus musculus centrin (Cetn2) gene, complete cds
7600	17451		1.15	2.8E-01	L13654.1	NT	Lycopersicon esculentum peroxidase (TPX1) mRNA, complete cds
7789	17639	27872	2.79	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
8126	18014	28261	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8126	18014	28262	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4109350 5'
8153	18041	28291	3.01	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
8254	18134	28382	2.62	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8599	18466		3.49	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
9552	19150		6.37	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
9667	19219	25236	3.11	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
9826	19651		1.69	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
597	10533	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	zx39b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1240	11147	20996	1.49	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1604	11509		1.73	2.7E-01	X79815.1	NT	G.lamblia SR2 gene
1698	11600	21471	2.96	2.7E-01	W58067.1	EST_HUMAN	zd22h10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1738	11639	21507	1.25	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2088	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2316	12197	22094	8.78	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2406	12283	22180	3.61	2.7E-01	AI310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element ;
2956	12883		1.25	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3929	13838	23618	1.88	2.7E-01	AI928015.1	EST_HUMAN	wo92e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3943	13851	23626	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4796	14681	24468	0.89	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs66) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4973	14848		3.5	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5221	15144	24838	3.49	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4)
6064	16047	26192	2.25	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6527	16386	26565	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566	2.23	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7378	17247	27453	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
7378	17247	27454	10.08	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS)
7379	17248		2.24	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
7801	17651	27888	1.29	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
7827	17677	27921	1.93	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATca) mRNA, complete cds
8187	18073	28322	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8187	18073	28323	1.76	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
8197	18082	28333	4.09	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9366	19034		1.27	2.7E-01	X95267.1	NT	G.gallus mRNA for ryanodine receptor type 3
9810	19320		2.15	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
462	12667	20224	1.54	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	10416		1.39	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1371	11277	21133	2.23	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1418	11324	21188	0.97	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	11750	21624	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	11750	21625	8.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
2046	11937		9.9	2.6E-01	AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2106	11995	21895	1.2	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2424	12301		2.68	2.6E-01	Y12996.1	NT	B.maritimus rbcL gene
2499	12374		9.68	2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
3053	12980		1.03	2.6E-01	AW974531.1	EST_HUMAN	EST386635 MAGE resequences, MAGM Homo sapiens cDNA
3485	13401		0.94	2.6E-01	BE217816.1	EST_HUMAN	hv30c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.t3 L1 repetitive element ;
3532	13448	23245	1.12	2.6E-01	M22342.1	NT	Bacteriphage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds

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Single Exon Probes Expressed in Heart

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3591	13505	23295	1.7	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23351	0.9	2.6E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23691	1	2.6E-01	AW959510.1	EST_HUMAN	EST371580 MAGE resequences, MAGF Homo sapiens cDNA
4062	13964	23742	13.13	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4259	14158	23935	0.95	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4548	14441	24224	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds
4616	14504	24292	1.28	2.6E-01	AF142703.1	NT	Ophrestia radicosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4896	14776	24564	3.56	2.6E-01	H04858.1	EST_HUMAN	yj51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5051	14923	24696	0.86	2.6E-01	P08503	SWISSPROT	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5700	19764		2.03	2.6E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
5763	15670	25777	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
5763	15670	25778	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 ;contains element LTR1 repetitive element ;
6552	16410	26588	1.52	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6585	16465	26656	1.27	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
6852	16731	26925	3.01	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150396 5'
6900	16779	26973	2.04	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 76.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
7046	16923	27112	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7046	16923	27113	4.34	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7854	17704		1.16	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18625		93.65	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9136	18892		1.98	2.6E-01	10190655	NT	Mus musculus jerky (Jrk), mRNA
9328	19655		1.92	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
9395	19053	25309	2.6	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9833	19333		6.03	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9899	19376		1.5	2.6E-01	Q01631	SWISSPROT	ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)
241	10209	20025	2.12	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025	1.86	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.5E-01	M26501.1	NT	Starfish (P.ochraceus) cytoplasmic actin gene, complete cds
815	10743	20589	1.32	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1044	10962		1.86	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20864	9.5	2.5E-01	T89837.1	EST_HUMAN	ye11g07.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1503	11407	21266	0.85	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1697	11599		5.43	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612	0.88	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1840	12706	21613	0.88	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2357	12237		8.29	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2446	12323		1.35	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2597	12466	22359	0.97	2.5E-01	X95310.1	NT	B.taurus mRNA for D-aspartate oxidase
3366	13285		2.87	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3490	13406	23211	0.86	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3502	13419	23220	7.93	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3774	13686	23468	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3774	13686	23469	1.15	2.5E-01	AI741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3977	13884		0.83	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120		1.2	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4514	14407	24193	0.96	2.5E-01	AF242431.1	NT	*Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9* and 11-16
4643	14531		1.14	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4649	14535	24324	3.78	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4672	14558	24351	2.19	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4698	14584		3.16	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4726	14612	24398	0.79	2.5E-01	BE896785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4760	14635	24421	0.89	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR
5169	15035	24802	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.t2 TAR1 repetitive element ;
5169	15035	24803	0.86	2.5E-01	AW663183.1	EST_HUMAN	hh75f09.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968649 5' similar to contains TAR1.t2 TAR1 repetitive element ;
5264	15186	24962	11.62	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6366	16229		1.32	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
6500	16359	26532	3.73	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6583	16463	26655	2.99	2.5E-01	BF109040.1	EST_HUMAN	7l57a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
6788	16667	26858	2.25	2.5E-01	BF038595.1	EST_HUMAN	601459238F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
7020	16897	27087	3.95	2.5E-01	H53236.1	EST_HUMAN	yq84f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
7481	17351	27554	16.11	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7481	17351	27555	16.11	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7522	17341	27547	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7522	17341	27548	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
7814	17664	27904	1.5	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
8010	17860	28105	1.62	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
8011	17861	28106	1.68	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
8426	18300	28556	2.32	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
9074	18851	29117	2.45	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA-4) mRNA, complete cds
9100	19729		4.2	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9559	19581	25072	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
541	10482	20292	1.53	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
830	10757	20608	2.38	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1282	11190	21041	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1282	11190	21042	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1362	11268	21123	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1808	11705		24.08	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1858	11754	21629	1.41	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	11980	21875	0.88	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2122	12010		1.16	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2216	12101	22005	2.01	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA O42586 26S PROTEASE REGULATORY SUBUNIT 6A ;
2491	12366	22260	1.63	2.4E-01	Z36534.1	NT	D.discoideum (Ax3-K) ponA gene
2734	12596	22491	2.14	2.4E-01	X71783.1	NT	S.pombe swi6 gene
2756	12618	22510	6.68	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3093	13020		2.82	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3109	13035	22831	1.85	2.4E-01	X74209.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
4817	14700	24486	0.88	2.4E-01	BE160080.1	EST_HUMAN	QV1-HT0412-020400-136-b10 HT0412 Homo sapiens cDNA
4981	14856	24622	50.15	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5469	15389	25451	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrn protein (Wrn) gene, complete cds
5469	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wrn protein (Wrn) gene, complete cds
5593	15508	25583	2.13	2.4E-01	BF592336.1	EST_HUMAN	7i54d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element ;
5642	15555	25648	2.66	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5705	15613	25714	2.15	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
5937	15842	25966	1.79	2.4E-01	AI698989.1	EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
6345	16208	26371	8.87	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
6860	16739	26931	1.62	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
7517	17305	27511	5.72	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22.b1 TAR1 repetitive element ;
7965	17815	28056	1.93	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
8149	18037	28285	3.63	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
8209	18093	28347	1.99	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
8534	18406		2.42	2.4E-01	Z21647.1	NT	P.asiatica mosaic virus genomic RNA
9030	18821	29109	1.55	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
9162	19526		2.39	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
9222	18945		2.64	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9439	19509		1.59	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
9650	19716		1.26	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
9865	19355		3.35	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
383	10330	20153	0.9	2.3E-01	S75898.1	NT	aromatase [Poephila guttata=zebra finches, ovary, mRNA, 3188 nt]

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
621	10558		4.42	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	10587	20403	19.84	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
918	10842	20687	3.35	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1494	11398	21258	1.5	2.3E-01	6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Vps4b), mRNA
1546	11451		0.88	2.3E-01	U22837.2	NT	Yersinia pestis HmsH (hmsH), HmsF (hmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1586	11490	21351	1.38	2.3E-01	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1614	11518	21378	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	11892		1.3	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2396	12274	22169	1.56	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2615	12483	22372	1.02	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2794	11271	21127	0.88	2.3E-01	AB015033.1	NT	Marinilabilia agarovorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2934	12861	22661	1.29	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element;contains element THR repetitive element ;
3046	12972		5.73	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3324	13244	23051	1.09	2.3E-01	H69836.1	EST_HUMAN	yr97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	13679	23461	1.11	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	13767		3.72	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926	0.85	2.3E-01	R82252.1	EST_HUMAN	yj17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4300	14198		3.35	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	14245	24031	1.02	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4386	14282	24061	2.08	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4956	14668	24455	0.82	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24641	0.95	2.3E-01	BF316135.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5101	14969	24745	0.98	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) *gene, RoRet gene, and sodium phosphate transporter* (NPT3) *gene, complete cds*
5146	15013	24783	26.95	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15169	24942	2.6	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074	1.71	2.3E-01	BF058381.1	EST_HUMAN	7k30b06.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5395	15314	25361	4.83	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5618	15533	25617	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5618	15533	25618	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16005	26142	3.93	2.3E-01	AI718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
6384	16246	26408	2.62	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6487	16345		3.19	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
6491	16349	26519	1.59	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
6560	16418		2.9	2.3E-01	N80983.1	EST_HUMAN	za12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292358 5'
6664	16544	26741	2.28	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7657	17507	27732	1.37	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
7712	17562	27787	2.54	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
7740	17590	27811	2.26	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
7974	17824		4.95	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
8525	18397	28663	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8525	18397	28664	2.84	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8658	18547	28830	2.39	2.3E-01	AE002167.2	NT	Chlamydophila pneumoniae AR39, section 4 of 94 of the complete genome
9144	18898		2.53	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
9232	18951		20.46	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCoE44 5'
9258	19477		1.65	2.3E-01	AA089819.1	EST_HUMAN	chn1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9266	18970		2.07	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
9324	19665	24990	2.05	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2. ;contains PTR5.b2 TAR1 repetitive element ;
9358	19708	24905	4.88	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
9407	19060		1.93	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
9456	19088		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19088		4.54	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9793	19310		2.67	2.3E-01	BF475611.1	EST_HUMAN	nac39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element ;

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
84	10068	19885	0.96	2.2E-01	AI052190.1	EST_HUMAN	oz14a10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
1545	11450	21311	3.13	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11865	-	0.91	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2042	11933	21829	2.78	2.2E-01	M34640.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2354	12234	22131	6.24	2.2E-01	BF677538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2543	12417	22307	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2543	12417	22308	2.41	2.2E-01	BE618258.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 6'
2853	12781	22570	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2853	12781	22571	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2890	12817		1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3346	13266		2.67	2.2E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	13655		1.05	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23688	0.81	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018		1.19	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4166	14066	23840	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4166	14066	23841	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4258	14157	23933	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4258	14157	23934	1.16	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4399	14294	24078	1.09	2.2E-01	Z54148.1	NT	B.abortus bp26 gene
4719	14605		1.22	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	14610	24396	2.47	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4891	14771	24549	1.19	2.2E-01	M86524.1	NT	Human dystrophin gene
4975	14850		1.2	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5513	15431	25495	1.71	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5518	15436		3.99	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6169	16074	26223	10.59	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
6676	16556		2.19	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7217	17094		2.29	2.2E-01	AW855039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
7304	17180	27382	1.39	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
7353	17221	27421	1.4	2.2E-01	W02988.1	EST_HUMAN	za04f08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291591 5'
7366	17344	27550	13.13	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522	3.98	2.2E-01	M89643.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
7648	17498	27720	3.57	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds; nuclear gene for chloroplast product
7719	17569	27794	2.2	2.2E-01	BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8723	18540	28824	4.94	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
8766	17906	28149	2.91	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
9077	18854		2.2	2.2E-01	BE870959.1	EST_HUMAN	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
9183	19720		3.72	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Ll>
9269	18973		2.34	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
9379	15093	24887	2.56	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9875	19713		3.75	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
955	10879	20727	1.74	2.1E-01	AA569289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
958	10881	20729	0.9	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1108	11023		2.16	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 46 of 85 of the complete genome
1180	11091	20936	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11767	21642	1.84	2.1E-01	AA906824.1	EST_HUMAN	ok73e02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02765 COMPLEMENT C3 PRECURSOR (HUMAN);
2111	12000	21899	3.08	2.1E-01	BF695073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2894	12821	22613	1.65	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3736	13648		5.05	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
3967	13874	23651	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
3967	13874	23652	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178		1.28	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4474	14368	24157	1.21	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4766	14651	24439	1.26	2.1E-01	AJ009794.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5134	15001	24772	0.99	2.1E-01	M98261.1	NT	Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds
5243	15167	24938	5.99	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6123	15970	26106	1.86	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
6386	16247		1.97	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6535	16393	26572	1.74	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
6559	16417	26596	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6559	16417	26597	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16585		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1l3), mRNA
6951	16829	27022	4.78	2.1E-01	U68399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
7224	17101	27289	5.88	2.1E-01	Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w
7479	17349	27553	2.36	2.1E-01	X97378.1	NT	A.thaliana mRNA for AtRanBP1b protein
7547	17398	27611	1.19	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
7917	17767	28006	2.49	2.1E-01	Z97067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
7929	17779	28018	1.49	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
8849	18661		2.31	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
8862	18674	28964	2.15	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA
9522	19132		1.6	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
9730	19634		1.4	2.1E-01	L32588.1	NT	Human granulin gene
9905	19382	25174	1.29	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
9979	19436		1.29	2.1E-01	5835904	NT	Salvelinus alpinus mitochondrion, complete genome
193	10165	19983	1.72	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds
523	10465		2.39	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
684	10617	20440	1.19	2.0E-01	M77085.1	NT	O.cunniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
793	10722	20563	1.81	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
996	10915	20759	1.03	2.0E-01	D90905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1109	11024	20866	2.57	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11141	20993	1.42	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1286	11194	21047	1.29	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1471	11376	21241	13.51	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	11442	21300	1.59	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1688	11590		1.82	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1723	11624		1.64	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
2299	12181		1.67	2.0E-01	X82877.1	NT	H.sapiens Na+-D-glucose cotransport regulator gene
2861	12789		0.95	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3442	13359	23166	0.8	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element ;
3646	13560	23346	0.81	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3945	13853	23628	0.8	2.0E-01	X83997.1	NT	C.parasitica eapC gene
4464	14358		8.47	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4859	14739	24519	1.07	2.0E-01	AF147083.1	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
4972	14847	24616	6.07	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5041	14913	24687	1.1	2.0E-01	Y19216.1	NT	Homo sapiens putative psihHbD pseudogene for hair keratin, exons 1 to 9
5342	15263	25089	2.55	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5510	15428	25491	2.13	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5694	15603	25705	5.29	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
5874	15780	25900	4.31	2.0E-01	X61033.1	NT	M.auratus mu class glutathione transferase gene
5934	15839	25962	3.64	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
6637	16517		6.95	2.0E-01	AF028026.1	NT	Andes virus strain Ol23133 glycoprotein G1 and G2 precursor, gene, partial cds
6772	16651	26839	4.18	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
7511	17299		4.39	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7692	17542		2.07	2.0E-01	AF146692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17624	27857	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
7774	17624	27858	1.95	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28350	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
8214	18098	28351	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9747	19308	25202	3.22	2.0E-01	AI023592.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
9769	19288		6.61	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9897	19374	25193	1.5	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k), mRNA
105	10086		10.35	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arnt1), mRNA
349	10308	20128	6	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
640	10577	20392	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
640	10577	20393	1.31	1.9E-01	U32581.2	NT	Homo sapiens lambda/iota protein kinase C-interacting protein mRNA, complete cds
647	10584	20400	5.37	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
648	10584	20400	7.32	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
970	10893		1.61	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1088	11004	20846	9.3	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1348	11254	21110	2.3	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322		3.91	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2330	12211	22109	3.31	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2892	12819	22611	3.91	1.9E-01	U66066.1	NT	Sigmodon hispidus p53 gene, partial cds
2908	12834		5.55	1.9E-01	J00922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3349	13269	23072	3.4	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	13351	23156	4.63	1.9E-01	R16467.1	EST_HUMAN	yf42f10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
3735	13647	23432	0.93	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
3762	13675	23457	0.96	1.9E-01	P39768	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3910	13820	23600	3.02	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
3992	13899	23676	1.89	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4138	14038	23813	1.06	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
4369	14265	24049	0.89	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4662	14548	24338	0.84	1.9E-01	Z93780.1	NT	Fugu rubripes genes encoding carbamoyl phosphate synthetase III, myosin light chain, MAP2
4912	14791	24566	0.86	1.9E-01	AW849203.1	EST_HUMAN	IL3-CT0215-180200-087-D02 CT0215 Homo sapiens cDNA
4943	14821		1.04	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
4962	14837	24605	1.11	1.9E-01	O95239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
5031	14903	24675	1.03	1.9E-01	AJ251176.1	NT	Phoca vitulina partial aar2B gene for alpha adrenergic receptor 2B
5113	14981	24755	0.99	1.9E-01	Z70296.1	NT	S.mansoni elastase HP1 gene
5123	14991		1.19	1.9E-01	AI631199.1	EST_HUMAN	ts93g12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2238886 3' similar to gb:M21574 ALPHA PLATELET-DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
5153	15020	24789	0.99	1.9E-01	6679095	NT	Mus musculus Notch gene homolog 3, (Drosophila) (Notch3), mRNA
5441	15361		4.28	1.9E-01	AW130149.1	EST_HUMAN	xf29a07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5466	15386	25446	7.67	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5588	15503		2.26	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6162	15119	24863	1.7	1.9E-01	R43212.1	EST_HUMAN	yg09a12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element ;
6423	16284	26446	1.43	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
6449	16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds
6658	16538	26735	1.62	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8038	17930	28176	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8038	17930	28177	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8137	18025	28271	1.76	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8961	18768	29060	2.61	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9546	19146		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
9880	19546		1.26	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
29	10016	19811	2.26	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
260	12663	20041	1.22	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
366	10322	20145	2.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	10661	20493	2.15	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
966	10889	20735	0.85	1.8E-01	AI912212.1	EST_HUMAN	wd71f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1075	10990	20832	1.21	1.8E-01	AF000580.1	NT	Dictyostelium discoideum plasmid Ddp5, complete genome
1267	11174	21024	5.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1487	11392	21252	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1487	11392	21253	1.29	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1803	11700		0.92	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	11720		1.93	1.8E-01	AI733708.1	EST_HUMAN	qg22d10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1873	11769	21644	1.6	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2660	12527		2.99	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-g04 DT0018 Homo sapiens cDNA
2868	12796		1.61	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2873	12800	22595	1.09	1.8E-01	AW182300.1	EST_HUMAN	xj41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3085	13012	22803	1.28	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3570	13484	23275	1.07	1.8E-01	H03369.1	EST_HUMAN	yj45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3570	13484	23276	1.07	1.8E-01	H03369.1	EST_HUMAN	yj45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4154	14054	23828	0.8	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4238	14137		1.13	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BoLA-DQB), complete cds
4456	14350	24141	5.12	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663	14549	24339	2.36	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4700	14586	24377	0.93	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4977	14852	24618	1.77	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5027	14900	24670	4.17	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	14925	24697	1.28	1.8E-01	AI439881.1	EST_HUMAN	ti57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5117	14985		1.03	1.8E-01	AJ000742.1	NT	Homo Sapiens hisH1 gene, 5' UTR
5549	15465	25535	1.41	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5922	15827	25952	1.29	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
5948	15853		2.5	1.8E-01	N94853.1	EST_HUMAN	yy62h02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6179	16065	26214	1.38	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
6179	16065	26215	1.38	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
7382	17251	27456	1.72	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.8E-01	9626232	NT	Bacteriophage Ike, complete genome
7933	17783	28022	1.19	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
8033	17925	28172	3.19	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	U38906.1	NT	Bacteriophage r1t integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
8118	16065	26214	2.9	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
8118	16065	26215	2.9	1.8E-01	AB018561.1	NT	Citrullus lanatus mRNA for wsus, complete cds
8119	18007	28254	3.88	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DG1041) gene, complete cds
8381	18258	28507	2.64	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
8758	17907	28152	3.98	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
8976	18781	29073	2.83	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbxa2r), mRNA
9169	18912	25344	1.65	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155318 5'
9625	19200		2.05	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9779	19294		1.63	1.8E-01	Y11114.1	NT	E.dispar mRNA for hexokinase (hxk1)
563	10503	20309	1.8	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
788	10717	20559	2.04	1.7E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
945	10870		1.89	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1042	10960	20802	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1042	10960	20803	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1938	11833		3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2829	12758	22548	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2829	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2898	12823	22616	1.74	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
2967	12894	22693	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctx-1 gene, exons 1-3
2967	12894	22694	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra ctx-1 gene, exons 1-3
3087	12994	22785	1.89	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3401	13318	23119	1.96	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3557	13471	23262	1	1.7E-01	AJ224877.1	NT	Homo sapiens hap1 gene, complete CDS
3859	13770	23562	4.41	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4459	14353		1.88	1.7E-01	X52936.1	NT	Schistocerca gregaria alpha repetitive DNA
4732	14617	24403	1.4	1.7E-01	AI247635.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR.b1 OFR repetitive element ;
4986	14861		1.16	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds
5067	14937		1.18	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme IIb (ae) gene, complete cds
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5820	15726	25839	12.31	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6112	16006		2.15	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6320	16183	26344	7.96	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6588	16468	26658	1.2	1.7E-01	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
6814	16693	26882	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6814	16693	26883	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
7066	16943	27135	2.46	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
7531	17382	27593	7.38	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
7601	17452	27666	2.06	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7942	17792	28032	1.48	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	nq60e07.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081 TRANSFORMING PROTEIN RHOC (HUMAN);
8067	17958	28208	9.13	1.7E-01	BE390835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
8182	18068	28317	2.47	1.7E-01	AA814617.1	EST_HUMAN	of43a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
8456	18329	28589	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8456	18329	28590	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8949	18757		1.92	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9012	18811	29107	4.38	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
9139	19666		1.5	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9420	19513		1.28	1.7E-01	AI824404.1	EST_HUMAN	tx69g05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
9705	19253	25218	5.79	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
120	10097	19917	1.88	1.6E-01	AF217532.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
664	12641	20416	1.53	1.6E-01	R31497.1	EST_HUMAN	yh75f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1505	11409	21268	4.05	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1882	11778	21653	2.4	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1941	11836		1	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2335	12719	22115	0.96	1.6E-01	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
2443	12320	22218	2.19	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22583	8.9	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2863	12791	22584	8.9	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23285	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3581	13495	23286	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3919	13828		2.61	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4234	14132	23908	7.92	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4353	14249		2.44	1.6E-01	AW968601.1	EST_HUMAN	EST380677 MAGE resequences, MAGJ Homo sapiens cDNA
4361	14257		4.01	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	14665	24451	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4781	14665	24452	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24524	1.14	1.6E-01	AA088343.1	EST_HUMAN	zl84h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221955 E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4869	14769	24546	1.92	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
4889	14769	24547	1.92	1.6E-01	AJ006356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
4958	14833	24601	1.09	1.6E-01	BE018707.1	EST_HUMAN	bb83h08.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715 TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
5390	15309	25162	3.12	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5390	15309	25163	3.12	1.6E-01	AW197496.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN ;
5398	15317	25364	2.07	1.6E-01	AF034716.1	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
5873	15779	25898	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
5873	15779	25899	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6157	15115	24858	3.7	1.6E-01	AW291215.1	EST_HUMAN	UI-H-BI2-agl-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
6571	16429	26612	1.84	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
6592	16472	26662	1.42	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7187	17064	27254	1.89	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
7564	17415		1.7	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
7565	17416	27631	1.91	1.6E-01	Z49501.1	NT	S.cerevisiae chromosome X reading frame ORF YJR001w
8049	17940	28190	2.71	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111189-028-G01 CT0220 Homo sapiens cDNA
8364	18241	28490	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8364	18241	28491	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8459	18332		7.6	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
8713	18530	28814	10.07	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
9001	18804	29097	2.69	1.6E-01	AW877127.1	EST_HUMAN	QV2-PT0010-160400-133-a08 PT0010 Homo sapiens cDNA
9026	19678		2.17	1.6E-01	6679466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
9141	18896	28795	2.33	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
9565	19493		6.33	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
9727	19265		2.84	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9807	19319		2.47	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19328	25208	1.27	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
248	10214	20030	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
766	10697	20534	1.4	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1076	10992	20834	0.88	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1081	10997	20838	1.87	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11108	20953	1.36	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1254	11161	21010	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1254	11161	21011	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1866	11762	21636	1.54	1.5E-01	AW444451.1	EST_HUMAN	UI-H-BI3-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2679	12544	22435	1.12	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2999	12927	22719	0.89	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22	1.5E-01	AA935049.1	EST_HUMAN	oo68d05.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433 RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3322	13242	23048	0.87	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3322	13242	23049	0.87	1.5E-01	Z23104.1	NT	L.stagnalis mRNA for G protein-coupled receptor
3380	13298	23097	0.96	1.5E-01	AW612237.1	EST_HUMAN	hh29f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element ;
3696	13610	23394	1.34	1.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35	1.5E-01	AW665983.1	EST_HUMAN	hj10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	13718	23506	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3806	13718	23507	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3964	13871	23649	0.96	1.5E-01	AW366659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4006	13912	23687	0.97	1.5E-01	Z12628.1	NT	B.napus mitochondrion DNA for ORF158
4091	13991	23768	8.36	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24301	1.34	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4645	12544	22435	2.18	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4680	14566	24361	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4680	14566	24362	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14808	24576	1.3	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.94	1.5E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	15139	24833	2.02	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5266	15188		5.67	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5400	15319	25367	4.06	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5424	15345	25398	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5424	15345	25399	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5652	15564	25660	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5652	15564	25661	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
5684	15593	25694	1.87	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5760	15668	25774	2.44	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
5785	15691		1.66	1.5E-01	4506396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
5828	15734	25845	1.78	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5917	19455	25948	1.96	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5935	15840	25963	5.13	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
5942	15847	25971	1.81	1.5E-01	P48508	SWISSPROT	GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5972	15876	26000	2.09	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6031	15935	26067	1.4	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6166	15123	24866	5.63	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
6284	16148		1.77	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16236	26396	1.88	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
6481	16340	26507	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.68	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6786	16665	26856	1.22	1.5E-01	AA970317.1	EST_HUMAN	oo85g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062 INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
6895	16774		11.77	1.5E-01	C16800.1	EST_HUMAN	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
6912	16790	26983	1.88	1.5E-01	L27835.1	NT	Pangasianodon gigas growth hormone (GH) mRNA, complete cds
6996	16873	27064	1.44	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7130	17007	27200	1.71	1.5E-01	4501972	NT	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
7265	17142	27335	2.48	1.5E-01	N74226.1	EST_HUMAN	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
7306	17182		2.98	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7706	17556	27781	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7706	17556	27782	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X98852.1	NT	P.leniusculus mRNA for integrin beta subunit
7908	17758	27998	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7908	17758	27999	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7939	17789	28031	1.54	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
8009	17859	28103	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8009	17859	28104	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8199	18084	28334	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8199	18084	28335	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8342	18219		1.74	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
8425	18299	28555	1.73	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
8506	16236	26396	2.17	1.5E-01	AI973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
9099	19547		20.02	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
9531	19565		4.14	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
9621	19588		2.14	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
9726	19497	25133	3.99	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
9932	19402	25179	3.01	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
9972	19432		1.58	1.5E-01	AF020346.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
296	10260		1.96	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S5P to TCRBV21S2A2 region
892	10818		2.57	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)-methyltransferase, complete cds
1238	11145		1.62	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	11615		1.43	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	11618	21487	1.53	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1863	11759		0.94	1.4E-01	AW135741.1	EST_HUMAN	UI-H-BI1-acf-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	11837		10.35	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2426	12303	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2762	12624	22517	3.07	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	R59232.1	EST_HUMAN	yg97a03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4083	13985	23762	8.38	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	23763	8.38	1.4E-01	AI699094.1	EST_HUMAN	tx56c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4313	14210		0.8	1.4E-01	AA776287.1	EST_HUMAN	zj50b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_rna1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu repetitive element;
5032	14904		0.91	1.4E-01	AW866022.1	EST_HUMAN	QV3-SN0022-100500-186-h09 SN0022 Homo sapiens cDNA
5116	14984	24759	1	1.4E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5147	15014	24784	0.81	1.4E-01	AJ005180.1	NT	Lycopersicon esculentum genomic RAPD band 26
5248	15171	24944	4.5	1.4E-01	T90677.1	EST_HUMAN	ye15c11.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5267	15189	24963	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	15189	24964	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5805	15710	25823	2.72	1.4E-01	BE326891.1	EST_HUMAN	hr67c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
5903	15809	25934	5.64	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	25935	5.64	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5958	15863	25985	3.07	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
5969	15874		1.56	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
5982	15887	26009	1.89	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
6371	16233		1.62	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BI0-aat-c-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6936	16814		1.33	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH06 3'
7167	17044	27236	4.48	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7300	17176	27377	8.05	1.4E-01	BF310959.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
7343	17211	27410	1.36	1.4E-01	W93411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element ;
7387	17256	27461	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7387	17256	27462	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7436	16449	26639	2.03	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducting adaptor protein (STAM), serine threonine kinase lal (IAL), and zinc finger protein (DNZ1) genes, complete cds
8091	17982		2.02	1.4E-01	AA811480.1	EST_HUMAN	oa99a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
8216	18100	28352	3.28	1.4E-01	R53400.1	EST_HUMAN	yj70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000890.1	NT	Ephydatia fluviatilis mRNA for aldolase, partial cds
9413	19065	25277	2.32	1.4E-01	X74773.1	NT	P.salina plastid gene secY
9427	19073		1.89	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
9560	19156		3.01	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycinamide ribonucleotide transformylase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
9646	19754		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19282		1.41	1.4E-01	BE782738.1	EST_HUMAN	601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868795 5'
9831	19332		1.42	1.4E-01	11425031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19566		3.41	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
9926	19398		1.77	1.4E-01	AW377998.1	EST_HUMAN	MR0-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281	20099	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	*Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK*
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
826	10753	20603	1.09	1.3E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20652	1.83	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20952	1.07	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'
1426	11331		1.36	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	12129		1.17	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.95	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3661	13575	23362	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3661	13575	23363	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3667	13581	23368	0.78	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodiol dehydrogenase 4 [AKR 1C4], exon 2
3714	13575	23362	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3714	13575	23363	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3734	13646	23431	0.85	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3906	13816		1.7	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4046	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4066	13968		3.44	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4075	13977	23756	1.89	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4093	13993	23770	16.36	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4192	14092	23870	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4192	14092	23871	0.85	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02 5'
4218	14116		1.65	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4433	14328	24116	2.16	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
4525	14418	24202	0.81	1.3E-01	BF679654.1	EST_HUMAN	602154306F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295544 5'
4771	15075		3.17	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'
4903	14783		0.86	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'
5074	14944	24718	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	14944	24719	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	15039	24805	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5173	15039	24806	0.9	1.3E-01	BF679819.1	EST_HUMAN	602154401F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'
5292	15213	25013	2.51	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5428	15348		1.79	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5904	15810	25936	13.21	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5956	15861	25983	2.04	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6305	16169		2	1.3E-01	H48664.1	EST_HUMAN	yr33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
6649	16529	26723	1.34	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6668	16548	26744	1.28	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
6858	16737		4.54	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
6886	16765		4.14	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
6960	16838	27031	1.27	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
7452	17261	27467	4.45	1.3E-01	AF023129.1	NT	Oryctolagus cuniculus H+,K+-ATPase alpha 2c subunit mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921		2.88	1.3E-01	BF330999.1	EST_HUMAN	MR4-BT0358-130700-010-h08 BT0358 Homo sapiens cDNA
8444	18318	28577	1.83	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576	18444		5.13	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cfl2), mRNA
8873	18685	28976	3.72	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
9261	18966	25320	1.97	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
9399	19054		3.18	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lymphotactin, exons 1-3
9757	19279		1.56	1.3E-01	AB026829.1	NT	Ephydatia fluviatilis mRNA for sALK-6, complete cds
9784	19297		1.32	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
9945	19414		1.26	1.3E-01	BF571764.1	EST_HUMAN	602078440F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4253049 5'
378	10362	20185	7.21	1.2E-01	AI421744.1	EST_HUMAN	tf39b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_rna1 ANNEXIN V (HUMAN);
418	9985		1.55	1.2E-01	U66912.1	NT	Dictyostelium discoideum ORF DG1016 gene, partial cds
535	10476		2.63	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1355	11261	21117	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1355	11261	21118	2.78	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1361	11267		3.94	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cdA Homo sapiens cDNA clone cdAAJB11 5'
1490	11395		1.13	1.2E-01	AA897474.1	EST_HUMAN	al48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1613	11517	21377	1.17	1.2E-01	Q14934	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1631	11535	21396	2.62	1.2E-01	AI285402.1	EST_HUMAN	qt69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1730	11631		29.48	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1877	11773		1.43	1.2E-01	AW449368.1	EST_HUMAN	UI-H-BI3-aki-e-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734564 3'
2134	12022	21919	2.1	1.2E-01	BF248490.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2240	12124	22025	1.01	1.2E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2546	12420	22310	2.02	1.2E-01	AW996556.1	EST_HUMAN	QV3-BN0046-220300-129-f10 BN0046 Homo sapiens cDNA
2697	12561	22451	0.86	1.2E-01	AI623388.1	EST_HUMAN	ts18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048 COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
2812	12741	22537	1.5	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2872	12799	22594	1.96	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L06095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2904	12831	22628	2.89	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.98	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	22923	2	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3219	13143		0.97	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350		0.79	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3477	13393	23198	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23199	1.14	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
3704	13617		0.88	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4090	13990	23766	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4090	13990	23767	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
5012	14886		1.04	1.2E-01	P16466	SWISSPROT	HEMOLYSIN PRECURSOR
5174	15040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5174	15040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME I
5199	15062		2.47	1.2E-01	AW401836.1	EST_HUMAN	UI-HF-BK0-aah-d-01-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617 5'
5251	15174	24947	2.63	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321699 5'
5297	15218	25021	1.9	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5762	15669	25776	1.69	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
5806	15711	25824	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
5839	15745	25858	1.56	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6607	16487		1.21	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-f09 BN0137 Homo sapiens cDNA
6642	16522	26715	2.46	1.2E-01	AI913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
6893	16772		9.72	1.2E-01	AW083652.1	EST_HUMAN	xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
6904	16782		3.88	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
7043	16920		2.27	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
7521	17340	27546	1.5	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
8260	18140		2.95	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
8417	18291		3.35	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
8487	18360		1.93	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8579	18447	28715	2.6	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8798	18612		2.02	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822		2.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
9383	19043		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
9458	19693	24897	2.58	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
9567	10476		7.69	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19230		1.41	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
9739	19706	24903	2.36	1.2E-01	BE061418.1	EST_HUMAN	QV4-BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9761	19281	25231	3.68	1.2E-01	AI299903.1	EST_HUMAN	qn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9782	19295		2.07	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19636		4.72	1.2E-01	O96433	SWISSPROT	CYCLIN T
9960	19424		2.18	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
552	10493	20301	0.95	1.1E-01	AI561003.1	EST_HUMAN	tn18d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
599	10535	20344	3.38	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_rna1 HEME OXYGENASE 1 (HUMAN);
1038	10956	20799	1.53	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1069	10985		1.29	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1143	12686	20899	4.06	1.1E-01	AW972158.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1229	11137	20990	1.72	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
1504	11408	21267	2.47	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2266	12150		2.25	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
2492	12653		1.17	1.1E-01	6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2520	12394		1.17	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2825	12754	22546	1.84	1.1E-01	S82418.1	NT	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
2997	12925	22717	0.8	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
3299	13221		1.39	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3374	13293	23092	3	1.1E-01	BE393186.1	EST_HUMAN	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3405	13322	23123	1.54	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3534	13450	23246	0.94	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3648	13562	23348	1.23	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4021	13925	23698	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA
4021	13925	23699	1.31	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0290-290100-025-g07 ST0290 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930		0.87	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, comple>
4159	14059		7.93	1.1E-01	AF157066.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4189	14089	23867	0.8	1.1E-01	AW802056.1	EST_HUMAN	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4466	14360	24150	0.91	1.1E-01	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4539	14432	24214	2.02	1.1E-01	S44957.1	NT	Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4725	14611	24397	1.26	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
4819	14702	24487	1.25	1.1E-01	D90908.1	NT	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
5479	15399		1.43	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element;contains element MER35 repetitive element ;
5562	15478	25551	1.54	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
5579	15494	25570	4.73	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5672	15581	25681	1.46	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
5687	15596	25697	1.79	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
5697	15606	25708	7.01	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
5876	15782	25903	1.39	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
5985	15890	26012	3.48	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME)
6027	15931		2.9	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6068	16052	26198	2.21	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
6448	16309	26474	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6448	16309	26475	7.05	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
6513	16372	26550	1.74	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
6531	16390	26570	3.07	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRANIN A PRECURSOR (HUMAN);
6777	16656	26845	1.57	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6777	16656	26846	1.57	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6803	16682	26872	1.22	1.1E-01	X91233.1	NT	H.sapiens IL15 gene
6826	16705		1.24	1.1E-01	AW817918.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
6862	16741	26934	1.78	1.1E-01	AL134349.1	EST_HUMAN	DKFZp547P194_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547P194 5'
7118	16995	27186	2.19	1.1E-01	U02482.1	NT	Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294	2.24	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7228	17105	27295	2.24	1.1E-01	AA192153.1	EST_HUMAN	zp93b12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
7287	17163	27362	2.48	1.1E-01	T72675.1	EST_HUMAN	yd19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7467	17327		2.08	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
7861	17711		1.23	1.1E-01	R80590.1	EST_HUMAN	yl96a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
8181	12925	22717	1.94	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
8294	18173		3.88	1.1E-01	AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
8402	18278	28530	2.93	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element;contains TAR1 repetitive element ;
8519	18391	28655	1.95	1.1E-01	X70058.1	NT	M.musculus cytokine gene
8539	18411	28676	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8539	18411	28677	3.21	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8626	18491	28763	2.79	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9241	18956		3.19	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
9485	19507		2.06	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
9893	19372	25192	2.14	1.1E-01	BF239753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1183	11094		4.08	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1251	11168	21007	1.89	1.0E-01	AI985499.1	EST_HUMAN	ws08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.t3 MER7 repetitive element ;
1370	11276	21132	2.88	1.0E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2439	12316	22213	1	1.0E-01	AW451365.1	EST_HUMAN	UI-H-BI3-alc-d-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3468	13384	23189	0.98	1.0E-01	BF033991.1	EST_HUMAN	601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3658	13572	23359	1.01	1.0E-01	BF239818.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3871	13782	23574	2.44	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4307	14204	23987	1.5	1.0E-01	AE002265.2	NT	Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome
4455	14349		1.17	1.0E-01	AI792349.1	EST_HUMAN	en32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4613	14501	24289	1.26	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4838	14719	24502	2.06	1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5158	15025	24792	0.87	1.0E-01	D49683.1	NT	Mouse FTZ-F1 gene
5188	15051	24815	1.44	1.0E-01	BF515935.1	EST_HUMAN	UI-H-BW1-aoa-e-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3'
5260	15182		9.16	1.0E-01	W86490.1	EST_HUMAN	zh62h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5670	15580	25680	11.21	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072		1.88	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
6549	16407		2.45	1.0E-01	Y12488.1	NT	M.musculus whn gene
7299	17176	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synamon mRNA, complete cds
7473	17333		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
7651	17501	27724	1.84	1.0E-01	BF240164.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17563	27788	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7713	17563	27789	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	28007	1.26	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 6'
8050	17941		2.02	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
8393	18269	28520	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8393	18269	28521	2.9	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18521	28803	4.43	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 6'
9226	19285		2.5	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9453	19085		1.34	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
9469	19098		2.03	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
9735	19688		2.57	1.0E-01	U52691.1	NT	Gonyaulex polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9765	19285		2.46	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9818	19664		8.59	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9871	19360	25187	1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for Toc34-2 protein (toc34B gene)
9877	19363		4.16	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2752	12614	22505	1.09	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2757	12619	22511	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2757	12619	22512	1.44	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2950	12877	22675	0.92	9.9E-02	AV730747.1	EST_HUMAN	AV730747 HTF Homo sapiens cDNA clone HTFBND05 5'
3229	13153	22952	1.15	9.9E-02	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
4582	14472	24260	22.55	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6161	15118	24862	7.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7332	17236	27440	1.5	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
551	10492		1.58	9.8E-02	X56338.1	NT	O.sativa RAmy3C gene for alpha-amylase
1711	11612	21482	1.53	9.8E-02	4503224	NT	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
3106	13032	22827	3.28	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	23805	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4131	14031	23806	6.67	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
8755	17904	28148	2.1	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
1328	11235	21092	1.16	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
3901	13811		3.56	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5661	15572	25669	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
6321	16184	26345	4.27	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2997771 to 3213410
6655	16535	26731	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
6655	16535	26732	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7137	17014	27207	1.32	9.7E-02	AI953984.1	EST_HUMAN	wx78b08.x1 NCI_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_rna1 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
8531	18403		1.97	9.7E-02	U58337.1	NT	Mus musculus ligatin (Lgtn) mRNA, partial cds
1969	11862	21753	1.27	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
1969	11862	21754	1.27	9.6E-02	AI080721.1	EST_HUMAN	oz47d11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4248	14147	23921	6.02	9.6E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4932	14810	24679	0.94	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
5093	14963	24738	0.8	9.6E-02	BE061729.1	EST_HUMAN	RC5-BT0254-031099-011-a03 BT0254 Homo sapiens cDNA
5713	15621		2.72	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
7502	17371	27580	1.51	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCAAH02 5'
7677	17527		1.84	9.6E-02	BE894895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
7772	17622	27855	1.75	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7772	17622	27856	1.75	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7839	17689	27933	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7839	17689	27934	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7886	17736	27980	3.29	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
8125	18013	28260	6.51	9.6E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
8957	18764	29056	1.8	9.6E-02	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
9798	19312		1.38	9.6E-02	H14599.1	EST_HUMAN	ym19h03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'
9848	19344	25212	1.26	9.6E-02	BE728219.1	EST_HUMAN	601563355F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'
4012	13918	23694	2.25	9.5E-02	AW992395.1	EST_HUMAN	CM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5062	14932	24704	0.87	9.5E-02	U63374.1	NT	Lycopersicon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6323	16186	26348	3.72	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
6467	16327	26494	7.46	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
6599	16479	26666	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
6599	16479	26667	2.59	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28206	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28207	3.29	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1792	11690	21565	3.86	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1820	11717	21597	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	11717	21598	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13716	23504	4.34	9.4E-02	Z33059.1	NT	M.capricolum DNA for CONTIG MC073
4980	14855	24621	0.89	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdbp), mRNA
6999	16876		2.62	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
8304	16338	26505	2.69	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vatI genes, complete cds, and Ipf35 gene, partial cds
9083	19603		3.36	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
9943	19411	25182	1.42	9.4E-02	U27699.1	NT	Human pephBGT-1 betaine-GABA transporter mRNA, complete cds
2960	12887		1.83	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
2993	12921		5.39	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3218	13142	22946	2.03	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4060	13962	23738	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4060	13962	23739	3.51	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4628	14516		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
7599	17450	27665	2.24	9.3E-02	BE962631.2	EST_HUMAN	601655988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
7855	17705	27949	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7855	17705	27950	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7913	17763		3.74	9.3E-02	AW206117.1	EST_HUMAN	UI-H-BI1-afx-h-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
9704	19555		8.62	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
9896	19602		1.95	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
228	10197	20008	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20009	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20010	4.32	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2180	12067		2.2	9.2E-02	R54156.1	EST_HUMAN	yg98f07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22866	4.53	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22986	1.16	9.2E-02	AA534354.1	EST_HUMAN	nf79e01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3537	13453		1.12	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
4145	14045		1.34	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4538	14431	24213	1.86	9.2E-02	X96402.1	NT	G.gallus Mia-CK gene
6670	16550	26746	1.86	9.2E-02	T49920.1	EST_HUMAN	ya99c09.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823	2.07	9.2E-02	X95256.1	NT	H.vulgare xylose isomerase gene
417	9984	19776	2.77	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
2365	12245	22139	1.01	9.1E-02	P78985	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
3618	13532		1.14	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161299-001-f02 BT0349 Homo sapiens cDNA
4383	14279	24058	1.81	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25487	1.73	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6372	16234	26393	11.89	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7958	17808		1.65	9:1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
9021	18815		1.29	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
9256	19692		1.52	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
9785	19548		5.63	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
727	10659	20490	3.36	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1617	11521	21379	6.45	9.0E-02	BE220482.1	EST_HUMAN	hv39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2772	12634	22528	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22529	1.11	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3294	13216	23018	0.92	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
4202	14101	23883	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23884	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4321	14218	24001	1.2	9.0E-02	P55268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4568	14460	24248	1.79	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	15009	24780	1.06	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
5647	15560	25653	8.02	9.0E-02	W56037.1	EST_HUMAN	za68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S52171 small G protein - human ;
9967	19428		15.35	9.0E-02	11431759	NT	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21189	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1419	11325	21190	2.15	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2338	12218	22117	1.41	8.9E-02	BE153572.1	EST_HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4534	14427	24208	0.92	8.9E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
5569	15485	25559	3.3	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5569	15485	25560	3.3	8.9E-02	AW452122.1	EST_HUMAN	UI-H-BI3-alo-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5576	15491	25568	3.13	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
6270	16135	26290	1.56	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320		1.83	8.9E-02	Z79021.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8
6998	16875	27066	5.28	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949		4.03	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
1351	11257	21113	1.25	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	23532	0.96	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
3948	13856		3.24	8.8E-02	O00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130)
4205	14104		1.13	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
7195	17072	27260	1.83	8.8E-02	AA151872.1	EST_HUMAN	zn99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
8461	18334	28596	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8461	18334	28597	3.19	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
8585	18453	28722	10.63	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1313 5'
9302	19001	25332	1.38	8.8E-02	Z71561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3636	13550	23337	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338	3.02	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3879	13790	23578	0.82	8.7E-02	W87841.1	EST_HUMAN	zh68a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:417194 5' similar to contains element MER12 repetitive element ;
4609	14497	24286	1.22	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.06	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5255	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
8094	17985		2.58	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
8631	18496	28770	1.77	8.7E-02	AJ007763.1	NT	Gluconobacter oxydans tRNA-Ile and tRNA-Ala genes
9293	18994		2.58	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9484	19105		1.81	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1232	11139	20991	7.05	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
2197	12084	21986	2.22	8.6E-02	BE408667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3151	13076	22876	2.94	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3593	13507		3.07	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenylyl cyclase (acrA) gene, complete cds
4385	14281	24060	0.87	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5708	15616	25718	4.38	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
5846	15752	25867	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
5846	15752	25868	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6628	16508	26695	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
6628	16508	26696	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8315	18192	28441	1.98	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192	28442	1.98	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28710	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8574	18442	28711	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
8738	17887	28131	4.71	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
8858	18670	28958	1.73	8.6E-02	AF283660.1	NT	Bacillus stearothermophilus BsrFI methylase (FIM) and BsrFI restriction endonuclease (FIR) genes, complete cds
2347	12227	22124	2.87	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5500	15419		1.8	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6658	15570	25665	5.34	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7003	16880	27072	1.93	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
7661	17511	27738	3.07	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
8498	18369		11.15	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
8512	18384	28649	4.07	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9681	19488		1.39	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9841	19339		3.28	8.5E-02	AA362934.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2632	12728	22391	4.24	8.4E-02	W69330.1	EST_HUMAN	zd44e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5253	15175	24949	7.82	8.4E-02	BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6019	15923	26053	1.71	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6680	16560	26755	8.11	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
7931	17781	28020	1.44	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312 O88312 GOB-4. ;
1965	11859	21748	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
1966	11869	21749	0.86	8.3E-02	5835680	NT	Ixodes hexagonus mitochondrion, complete genome
3544	13460	23254	6.19	8.3E-02	P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	13481	23271	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3567	13481	23272	0.88	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5840	15746	25859	2.82	8.3E-02	AF052683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6653	16533	26728	3.42	8.3E-02	AF195787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
6671	16551		1.47	8.3E-02	AA865285.1	EST_HUMAN	og88g08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 repetitive element ;
6829	16708		1.42	8.3E-02	AA987873.1	EST_HUMAN	oq81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
7498	17368	27573	1.44	8.3E-02	AW583503.1	EST_HUMAN	ia05h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;
7506	17294		1.94	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
9307	19695		1.55	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'
1357	11263		7.82	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1480	11385	21248	1.21	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3036	12964		1.78	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3733	13645		1.26	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3926	13835	23615	1.11	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23862	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23863	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23864	5.36	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	24655	2.82	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5271	15193	24968	1.43	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
6188	16073	26222	3.14	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
7536	17387	27598	5.33	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
7628	17479	27699	2.11	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
9314	19006	25336	4.13	8.2E-02	AE002246.2	NT	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome
9706	19480		1.84	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
7703	17553		1.65	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
8789	18604	28894	3.38	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5	12657	19784	3.28	8.0E-02	AW954653.1	EST_HUMAN	EST366723 MAGE resequences, MAGC Homo sapiens cDNA
920	10844	20690	1.33	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1671	12701	21440	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1671	12701	21441	10.54	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1861	11757	21632	3.9	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2323	12204	22103	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2323	12204	22104	1.01	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2421	12298		4.08	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2790	10991	20833	0.81	8.0E-02	M23449.1	NT	Dictyoselium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2870	12797	22591	1.01	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3745	13658	23440	0.84	8.0E-02	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
3980	13887		1.06	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4709	14595		5.62	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
4834	14716	24499	0.87	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene,s complete cds, and small nuclear RNAs (uRNAs)
5591	15506	25581	3.35	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6261	15506	25581	1.63	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6727	16607	26798	3.65	8.0E-02	AL114893.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7401	17268	27471	1.49	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
7401	17268	27472	1.49	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	25300	2.94	8.0E-02	AJ005375.1	NT	*Drosophila orena* hunchback region
9891	13887		1.47	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9969	19654		3.04	8.0E-02	AJ278435.1	NT	Mus musculus Ranbp7 gene, Staf gene and Wee1 gene
2127	12015	21913	3.98	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
2948	12875	22673	6.43	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	23471	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3776	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4595	14483	24269	1.06	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155401 5'
4706	14592		1.16	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6682	16562	26756	3.25	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smt4p (SMT4) gene, complete cds
7762	17612	27838	5.68	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
7762	17612	27839	5.68	7.9E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
1192	11102	20947	1.43	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
1192	11102	20948	1.43	7.8E-02	AI793275.1	EST_HUMAN	oo59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.t3 L1 repetitive element ;
4688	14574	24371	0.81	7.8E-02	BE836331.1	EST_HUMAN	PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
5019	13603		2.71	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
5197	15060	24825	1.04	7.8E-02	AI418520.1	EST_HUMAN	tg48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.t3 MER10 repetitive element ;
7236	17113	27306	2.06	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
7236	17113	27307	2.06	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
7389	17307	27613	1.27	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
1378	12693	21139	1	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3538	13454		2.09	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6615	16495	26682	4.4	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ;

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7660	17510	27736	4.62	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
8376	18253	28504	5.24	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
9535	19561		2	7.7E-02	11436859	NT	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3362	13281	23081	0.94	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3512	13428	23229	0.93	7.6E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.96	7.6E-02	AW858844.1	EST_HUMAN	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
7393	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
7695	17545		1.34	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
8927	18735	29028	2.45	7.6E-02	AW996645.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20536	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4407	14301	24085	0.84	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
6855	16734	26927	1.19	7.5E-02	AI864367.1	EST_HUMAN	wl52b02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
6953	16831	27024	1.21	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
469	10412	20231	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1444	11349		1.08	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	12410		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pitx1), mRNA
3545	13461	23255	0.89	7.4E-02	AI807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4606	14494	24282	3.38	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4687	14573	24370	2.66	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
4858	14738	24618	1.7	7.4E-02	6678492	NT	Mus musculus ubiquintin c-terminal hydrolase related polypeptide (Uchrp), mRNA
5913	15819		1.75	7.4E-02	R17477.1	EST_HUMAN	yg14g06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
6612	16492	26678	1.4	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
6950	16828	27021	1.37	7.4E-02	U56089.1	NT	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9271	18975		2.08	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
9527	19674		2.82	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
9678	19235	25242	1.81	7.4E-02	BF035099.1	EST_HUMAN	601453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
461	10405	20222	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
461	10405	20223	0.96	7.3E-02	BE964961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
669	10603	20420	2.73	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1465	12695	21237	3.04	7.3E-02	AW900281.1	EST_HUMAN	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1801	12705		14.81	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	14806		1.01	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6413	16275	26437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6413	16275	26438	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16628		1.27	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8548	15788	25910	2.78	7.3E-02	AA779977.1	EST_HUMAN	zj24a02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19911	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	10093	19912	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1460	11365	21228	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1460	11365	21229	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12377		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3810	13722	23511	0.82	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BW0-ajl-a-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'
4249	14148	23922	4.02	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4594	14482	24268	78.82	7.2E-02	11466563	NT	Rhodomonas salina mitochondrion, complete genome
4997	14872	24636	0.94	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24922	3.03	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24923	7.62	7.2E-02	P11120	SWISSPROT	CALMODULIN
6252	16118	26272	9.33	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
6281	16145		1.75	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
7646	17396	27608	2.05	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
7625	17476	27697	4.23	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
7746	17596	27818	2.64	7.2E-02	AW873187.1	EST_HUMAN	hq24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
7926	17776	28016	2.05	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Single Exon Probes Expressed in Heart

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7983	17833	28073	5.47	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
7994	17844		3.2	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
9178	18919	25346	1.44	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
9214	18942		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D6 3'
9273	18977		1.44	7.2E-02	AA584465.1	EST_HUMAN	no05h08.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
9332	19013		1.62	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
9346	19531		3.89	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
1862	11758	21633	1.65	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome
2247	12131	22028	5.08	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
9063	18844		4.98	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
517	10459	20270	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1484	11389		1.46	7.0E-02	X96677.1	NT	M.artiellia Mtcut-1 gene
1725	11626	21495	1.36	7.0E-02	AA056343.1	EST_HUMAN	zl66f04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
2994	12922	22715	1.72	7.0E-02	AW138152.1	EST_HUMAN	UI-H-BI1-acy-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3822	13734	23523	1	7.0E-02	AA815438.1	EST_HUMAN	ai65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
3958	13866	23642	1.24	7.0E-02	BE070264.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4047	13949		1.08	7.0E-02	AW792962.1	EST_HUMAN	CM0-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
4121	14021	23799	1.27	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4846	14727	24510	7.1	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7259	17136	27329	1.25	7.0E-02	9628113	NT	African swine fever virus, complete genome
7634	17385	27597	1.19	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
8679	18567	28850	2.39	7.0E-02	AA724295.1	EST_HUMAN	ah99a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837 TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
503	10445	20256	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
503	10445	20257	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1311	11217		1.31	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3724	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3724	13636	23422	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	14988		1.05	6.9E-02	AF079906.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6978	16855	27048	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
6978	16855	27049	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9208	18939		3.95	6.9E-02	X74316.1	NT	X.laevis XFD2 mRNA for fork head protein
9385	19045		1.5	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
9598	19180		2.19	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1839	11736	21610	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1839	11736	21611	1.11	6.8E-02	AA496759.1	EST_HUMAN	ae30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382 MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1865	11761	21635	3.91	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
3062	12989	22780	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22781	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22782	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	14347		0.92	6.8E-02	BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6315	16178	26337	7.71	6.8E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6822	16701	26894	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
6822	16701	26895	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9011	19719		1.37	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3'end similar to LINE-1
9140	18895		2.98	6.8E-02	AA758014.1	EST_HUMAN	ah67f05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
9764	19284		2.97	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1511	11416		2.17	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1851	11747	21622	2.5	6.7E-02	AI220285.1	EST_HUMAN	qg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3656	13570	23356	3.52	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOX-A)
1326	11233	21089	1.05	6.6E-02	AI735509.1	EST_HUMAN	at12e09.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
1347	11253	21109	1.5	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2133	12021	21918	3.07	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcipts
3133	13058		1.32	6.6E-02	Q13585	SWISSPROT	MELATONIN-RELATED RECEPTOR (H9)
3418	13335	23139	8.61	6.6E-02	R64306.1	EST_HUMAN	yi18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3432	13349	23154	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3432	13349	23155	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3989	13896	23673	1.59	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4904	14784	24558	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5167	15033	24800	1.34	6.6E-02	AF204882.1	NT	Amsacta albistriga nucleopolyhedrovirus AcORF17 homolog gene, complete cds
5190	15053	24817	0.84	6.6E-02	AE004345.1	NT	Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome
5968	15873	25998	3.09	6.6E-02	X06411.1	NT	P.vulgaris mRNA for chalcone synthase
6209	15969	26105	2.93	6.6E-02	AI243326.1	EST_HUMAN	qh41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'
6635	16515	26706	1.48	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7806	17656	27894	1.37	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
8330	18207	28457	6.28	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-006-e12 SN0064 Homo sapiens cDNA
9593	19175		2.08	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
9882	19366		1.46	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
567	10506	20313	1.91	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
971	10895	20743	1.75	6.5E-02	7706068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1369	11275	21131	4.17	6.5E-02	U47624.1	NT	Xenopus laevis *alpha*(E)-catenin mRNA, complete cds
1702	11603	21474	2.16	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
5413	15333	25383	1.76	6.5E-02	AA443991.1	EST_HUMAN	zv46h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
8035	17927	28173	5.61	6.5E-02	AA195648.1	EST_HUMAN	zr32g05.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
9034	18823		3.53	6.5E-02	M21496.1	NT	Rabbit microsomal epoxide hydrolase
9393	19051		3.73	6.5E-02	AF102993.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
561	10501	20307	1.53	6.4E-02	X94549.1	NT	A.carterae precursor of peridinin-chlorophyll-protein (PCP) gene
4802	12909	22708	1.35	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5180	15044		8.78	6.4E-02	6996923	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
5346	15267	25094	1.4	6.4E-02	AI191956.1	EST_HUMAN	qe07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element ;
5718	15625	25727	7.58	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
5718	15625	25728	7.58	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6079	16062	26210	5.23	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
6853	16732		2.57	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (*zeta*) (Cct6a), mRNA
7034	16911	27099	4.12	6.4E-02	AA093305.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
7603	17454	27668	2.02	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
8946	18754	29049	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8946	18754	29050	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9289	19635		3.65	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
9337	19017	25295	2.27	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1720	11621	21490	2.43	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3552	13467		2.09	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17602	27825	3.14	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
8098	15637	25741	3.29	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
9373	19039		1.49	6.3E-02	P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4157	14057	23831	3.37	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4243	14142		1.11	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4479	14373		5.41	6.2E-02	Q62191	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
4803	14687		1.22	6.2E-02	AV705701.1	EST_HUMAN	AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5'
7459	17319	27525	1.21	6.2E-02	6677898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
8655	18544	28827	1.84	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
9129	19752		3.53	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
9541	19142	25265	1.98	6.2E-02	BF112039.1	EST_HUMAN	7l37h08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1] ;
256	10222	20038	4.53	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3909	13819		2.65	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKC1) gene, complete cds
5150	15017	24785	1.01	6.1E-02	AB040897.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
6809	16688	26877	3.46	6.1E-02	X99268.1	NT	H.sapiens mRNA for B-HLH DNA binding protein
8112	18002	28248	5.44	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA
9088	19670		7.17	6.1E-02	X70969.1	NT	S.japonicum mRNA for serine-enzyme
9783	19296		3.6	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1241	11148	20997	1.41	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2641	12508	22399	1.57	6.0E-02	AW968848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2745	12607		1.61	6.0E-02	AB031289.1	NT	Mesocestoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2906	10076	19892	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2906	10076	19893	1.22	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3191	13116	22921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma.IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3583	13497		0.9	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5314	15235		3.46	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6172	15129	24848	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6172	15129	24849	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
6265	16130	26284	1.97	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
6524	16383	26562	2.05	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
7340	17208	27406	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7340	17208	27407	1.19	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17278	27486	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
7411	17278	27487	1.79	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9336	19016	25294	1.95	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
9715	19256		1.84	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 O60298 KIAA0551 PROTEIN ;
229	10198	20011	3.42	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
2955	12882	22681	2.59	5.9E-02	AF190269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4770	14655	24443	0.88	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7008	16885	27077	1.87	5.9E-02	9055249	NT	Mus musculus iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
8165	18053		2.72	5.9E-02	6679870	NT	Mus musculus follistatin-like (Fstl), mRNA
8383	18260	28509	3.15	5.9E-02	11433356	NT	Homo sapiens ninein (LOC51199), mRNA
8842	18655		1.99	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
917	10841		4.35	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2830	12759		1.1	5.8E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3613	13527	23314	1.44	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4257	14156	23931	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4257	14156	23932	4.36	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132	4.21	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4447	14341	24133	4.21	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	14365		2.04	5.8E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6523	16382	26560	2.79	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
6523	16382	26561	2.79	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9227	18948		2.34	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
9518	19739		4.56	5.8E-02	AA604269.1	EST_HUMAN	no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3018	12946	22738	1.34	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2 CE08611 ;
3033	12961	22754	1.34	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3731	13643	23428	1.8	5.7E-02	AW966791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
6740	16619	26808	1.42	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
8524	18396	28661	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
8524	18396	28662	3.86	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
9437	19558		5.55	5.7E-02	D50320.1	NT	Pig DNA for SPAI-2, complete cds
9662	19630		2.47	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
9796	19727		3.82	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1510	11415	21274	0.86	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
4540	14433	24215	1.26	5.6E-02	AB013100.1	NT	Lycopersicon esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4598	14486	24272	1.14	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
6008	15913	26040	4.74	5.6E-02	AW172708.1	EST_HUMAN	xj02c10.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0905 PROTEIN. ;
6241	16107	26258	2.88	5.6E-02	BE008001.1	EST_HUMAN	QV0-BN0147-290400-214-g07 BN0147 Homo sapiens cDNA
7110	16987	27178	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7110	16987	27179	2.29	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
7647	17497	27719	1.15	5.6E-02	AA482864.1	EST_HUMAN	nf49d07.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C. ;
8850	18662		2.18	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2618	12486	22375	8.16	5.5E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3179	13104	22909	3.6	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4777	14661	24448	0.81	5.5E-02	AF161266.1	NT	Murray Valley encephalitis virus strain MVE-1-51, complete genome
5472	15392	25456	3.47	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5671	15392	25456	4.31	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6365	16228	26388	1.58	5.5E-02	6755902	NT	Mus musculus tuftelin 1 (Tuft1), mRNA
7566	17417	27632	1.3	5.5E-02	10947034	NT	Homo sapiens elF4E-transporter (4E-T), mRNA
7566	17417	27633	1.3	5.5E-02	10947034	NT	Homo sapiens elF4E-transporter (4E-T), mRNA
7619	17470	27689	1.48	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
8382	18259	28508	11.56	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB),>
2986	12914		0.95	5.4E-02	AJ277468.1	NT	Oryza sativa rbbi3-1 gene for putative Bowman Birk trypsin inhibitor
3376	15078		6.34	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
4908	14787	24563	0.92	5.4E-02	U53528.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
5108	14976	24751	1	5.4E-02	M96761.1	NT	Mus musculus p-glycoprotein (mdrla) gene, exons 1 and 2
8083	17974	28223	1.79	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
9323	19552		1.55	5.4E-02	U44894.1	NT	Rana catesbiana heat shock protein 30 (HSP30) mRNA, complete cds
1037	10955	20797	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1037	10955	20798	1.62	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1489	11394	21255	18.21	5.3E-02	T94759.1	EST_HUMAN	ye37f12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2447	12324	22222	3.14	5.3E-02	AJ276408.1	NT	Pseudomonas putida ttgS gene
2912	12839	22638	3.91	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
2912	12839	22639	3.91	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3113	13038	22834	4.59	5.3E-02	AJ276408.1	NT	Pseudomonas putida ttgS gene
4506	14399	24185	1.22	5.3E-02	AJ011048.1	NT	Arabidopsis thaliana eli5 gene, exons 1-11
5021	14894	24662	7.26	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
6258	15180	24955	1.76	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5258	15180	24956	1.76	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6115	16009	26145	3.87	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
6353	16216		1.94	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7276	17153	27349	1.78	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
2239	12123		439.66	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3076	13003	22793	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3076	13003	22794	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4181	14081	23854	3.35	5.2E-02	U07132.1	NT	Human steroid hormone receptor Ner-I mRNA, complete cds
4633	14521	24311	1.04	5.2E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sep1) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5714	15622		1.73	5.2E-02	AI830965.1	EST_HUMAN	wj80e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element ;
6768	16647		2.23	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
7610	17461	27677	2.03	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
7610	17461	27678	2.03	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9561	19157		1.63	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
2313	12194		1.02	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D073 5'
4979	14854	24620	1.12	5.1E-02	BE957423.2	EST_HUMAN	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6098	16108	24871	1.65	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
6859	16738	26930	1.43	5.1E-02	AJ131966.1	NT	Spodoptera littoralis mRNA for 3-dehydroecdysone 3beta-reductase
7645	17495	27716	6.22	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
7849	17699	27944	2.36	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
8204	18088	28339	2.42	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
8204	18088	28340	2.42	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
9569	19169		1.81	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
474	10418	20234	1.98	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1186	11096	20942	7.11	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
1947	11842	21726	4.27	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2788	10894	20742	1.64	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3295	13217		1.17	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3629	13543	23330	5.63	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
4890	14770	24548	0.88	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetratricopeptide containing protein RoXaN mRNA, partial cds
6450	16311	26477	10.61	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7858	17708	27954	1.32	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
8782	18597	28886	2.47	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
9096	19593		2.81	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
218	10188		28.95	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
365	10321	20143	2.57	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
365	10321	20144	2.57	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3251	13174	22972	1.87	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN)
3522	13438		0.87	4.9E-02	AA188940.1	EST_HUMAN	zq48e12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
3543	13459	23252	1.19	4.9E-02	AA400914.1	EST_HUMAN	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3543	13459	23253	1.19	4.9E-02	AA400914.1	EST_HUMAN	zt78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4733	14618	24404	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'
4733	14618	24405	1.89	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632386 3'
5299	15220	25023	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5299	15220	25024	1.94	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
8705	18523	28805	3.78	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
9490	19107		2.26	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
9751	19276		3.67	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
327	10287	20104	1.45	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
328	10287	20104	1.97	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
480	10424	20239	7.54	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2227	12112	22014	1.92	4.8E-02	W51983.1	EST_HUMAN	zc49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3172	13097	22903	2.12	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4572	14464		1.67	4.8E-02	Z54280.1	NT	S.scrofa gene for skeletal muscle ryanodine receptor
5076	14946	24722	1.28	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
6731	16611	26801	1.31	4.8E-02	AW388497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
4940	14818	24586	0.78	4.7E-02	6981261	NT	Rattus norvegicus Nestin (Nes), mRNA
6085	16030	26170	3.41	4.7E-02	W01153.1	EST_HUMAN	yz97f09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
6134	15981	26117	1.65	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
6800	16679	26868	9.71	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
7179	17056	27245	1.18	4.7E-02	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
7189	17066		2.63	4.7E-02	AB026678.1	NT	Gallus gallus Wpkci-8 gene, complete cds
7321	17197	27397	7.44	4.7E-02	X15543.1	NT	B.taurus mRNA for RF-36-DNA-binding protein
8136	18024	28270	1.76	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
9305	19740		2.35	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
9652	19743		2.35	4.7E-02	P52951	SWISSPROT	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
9881	19365		1.39	4.7E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
722	10654	20484	2.74	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1270	11177		1.06	4.6E-02	AI014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533 P90533 LIMA ;contains element LTR1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1336	11242	21100	2.74	4.6E-02	AV727059.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
2438	12315	22212	2.51	4.6E-02	AW236023.1	EST_HUMAN	xn24f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1 ;
2777	10235	20052	1.51	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
2977	12904	22703	0.98	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3451	12904	22703	0.95	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4033	13936		1.22	4.6E-02	AF220365.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddx21) gene, complete cds
5777	15684	25792	3.64	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
5777	15684	25793	3.64	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6070	16053	26200	1.31	4.6E-02	AI149574.1	EST_HUMAN	qc60b06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.t3 L1 repetitive element ;
7029	16906	27097	3.65	4.6E-02	BE154006.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
8707	18524	28806	3.58	4.6E-02	AA913328.1	EST_HUMAN	ol27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
9633	19738		1.34	4.6E-02	L11692.1	NT	Oryctolagus cuniculus macrophage scavenger receptor type II mRNA, complete cds
9845	19343		2.68	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
439	10383	20207	1.84	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1200	11110	20955	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1200	11110	20956	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozolin VP35 gene, complete cds
1763	11662	21535	3.55	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2063	11953	21850	2.04	4.5E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3662	13576	23364	3.83	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5778	15685	25794	1.54	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6891	16770	26965	2.3	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
7718	17568	27793	4.43	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to similar to neuro-D4 protein
9301	19000	25331	1.74	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFPL3), mRNA
9691	19637	25009	3.41	4.5E-02	AA191097.1	EST_HUMAN	zq43f11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
213	10184		4.79	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
1008	10926	20770	1.29	4.4E-02	L19295.1	NT	Drosophila melanogaster extradenticle (EXD) mRNA, complete cds
2049	11940		6.15	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2440	12317	22214	1.29	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
3588	13502	23291	1.88	4.4E-02	AF159160.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4527	14420	24203	1.08	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4527	14420	24204	1.08	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4637	14525		3.12	4.4E-02	AJ222689.1	NT	Ovis aries CCAAT-enhancer binding protein epsilon gene
7084	16961	27154	1.96	4.4E-02	AA736969.1	EST_HUMAN	nw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
8423	18297	28552	4.11	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
8533	18405	28670	2.39	4.4E-02	AA496739.1	EST_HUMAN	ae33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
9029	18820		1.88	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
9210	19753		1.44	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
764	10695	20532	5.74	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2521	12395	22286	1.23	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3383	13301	23101	7.04	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3609	13523		1.07	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
5141	15008	24779	0.92	4.3E-02	X51594.1	NT	Pea P4 organ specific gene
5914	15820	25944	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
5914	15820	25945	4.93	4.3E-02	P30427	SWISSPROT	PLECTIN
8242	18122	28372	2.48	4.3E-02	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
805	10734	20577	2.05	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
848	10775		1.93	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
878	10804	20654	0.83	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291 L1 RETROPOSON, ORF2 MRNA ;contains L1.t3 L1 L1 repetitive element ;
1690	11592		1.21	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
3117	13042	22838	0.9	4.2E-02	AI493472.1	EST_HUMAN	qy95f10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718 FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN);
5172	15038		1.07	4.2E-02	D63484.1	NT	Human mRNA for KIAA0150 gene, partial cds
6444	16305	26470	4.45	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7114	16991	27183	3.88	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7845	17695	27941	1.28	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
8627	18492	28764	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8627	18492	28765	2.33	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
8795	18609	28900	1.73	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
9563	19881		2.69	4.2E-02	AI983494.1	EST_HUMAN	wt49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
2643	12510	22401	0.97	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
3824	13736	23526	0.86	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3824	13736	23527	0.86	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4372	14268		7.37	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-164-f06 NN0012 Homo sapiens cDNA
6436	16297	26459	1.84	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
6565	16423	26604	2.44	4.1E-02	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
9873	19682	24994	12.83	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
3206	13130	22932	2.68	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5304	15225	25029	4.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6528	16387	26567	5.69	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7059	16936	27126	2.8	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572	17423	27638	2.42	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A
8983	18788		1.94	4.0E-02	AJ001018.1	NT	Kluyveromyces lactis gene for Ca++ ATPase
9196	19506	25135	4.96	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1104	11020	20863	2.77	3.9E-02	BF516149.1	EST_HUMAN	UI-H-BW1-anx-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1322	11229	21084	3.46	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
1918	11813	21691	3.04	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2671	12536		2.29	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5105	14973	24748	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5105	14973	24749	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
6581	16461	26654	1.22	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
9056	19644		5.45	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
9697	19248		1.57	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
9811	19568		7.38	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
1909	11804	21683	0.94	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6331	16194	26355	1.74	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7033	16910		1.39	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
8045	17936	28185	2.45	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10899	20746	4.59	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	11272	21128	0.9	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	12077	21982	6.3	3.7E-02	AI984806.1	EST_HUMAN	wr85e08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2533	12407	22299	0.91	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3012	12940	22733	0.8	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3013	12941	22734	3.45	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3408	13325		1.1	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
9095	18867	29119	3.4	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
9755	19539	25063	1.62	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3604	13518	23306	0.85	3.6E-02	X73221.1	NT	H.vulgare Ss1 gene for sucrose synthase
3612	13526	23313	0.8	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5135	15002	24773	0.84	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
6028	15932	26062	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6028	15932	26063	5	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6214	16080	26229	1.82	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds
6324	16187	26349	2.63	3.6E-02	AA714521.1	EST_HUMAN	nw20e05.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
7402	17269	27473	2.08	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
877	10803	20653	1.15	3.5E-02	U09506.1	NT	Drosophila melanogaster tiggrin mRNA, complete cds
992	10913	20758	1.53	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21309	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1544	11449	21310	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4120	14020	23798	2.01	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4220	14118	23895	1.43	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4536	14429		0.96	3.5E-02	AW958469.1	EST_HUMAN	EST370539 MAGE resequences, MAGE Homo sapiens cDNA
5154	15021		0.84	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-CPA2 INTERGENIC REGION
5773	15680	25787	1.88	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
7012	16889	27082	2.35	3.5E-02	BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
7755	17605	27829	1.72	3.5E-02	X76642.1	NT	L.lactis MG1363 grpE and dnaK genes
8786	18600	28889	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
8785	18600	28890	1.76	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
9749	19582		3.51	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
564	10504	20310	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
564	10504	20311	1.78	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20310	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
565	10504	20311	3.31	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1035	10953	20795	3.77	3.4E-02	AW274020.1	EST_HUMAN	xv26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1188	11098		10.22	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2343	12223	22120	2.06	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3384	13302	23102	1.25	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3709	13622	23405	1.07	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3845	13756	23550	3.18	3.4E-02	AW794952.1	EST_HUMAN	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4494	14388	24174	2.41	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
4992	14867		3.43	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5010	14884	24650	1.28	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6095	15105	24868	4.19	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
6808	16687		4.78	3.4E-02	AI869629.1	EST_HUMAN	wi99d04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433031 3'
7169	17046		6.07	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425 IPISGKPLPKVTLSRDGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAANSSGTTKAFINIVVLDRPG PPT GPVVISDITEESVTLKWEPPKYDGGSQVTNYILLKRETSTAVWTEVSATVARTMMKVMKL ... ;
368	10324		13.18	3.3E-02	AA398735.1	EST_HUMAN	zt75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1151	11064	20907	13.17	3.3E-02	AB035867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1621	11525	21383	1.08	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1705	11606		1.28	3.3E-02	AE000700.1	NT	Aquifex aeolicus section 32 of 109 of the complete genome
2038	11929		2.77	3.3E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4086	11525	21383	2.24	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4366	14262	24047	1.88	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
5875	15781	25901	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
5875	15781	25902	18.26	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8464	18337	28601	3.39	3.3E-02	BF691107.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
9290	18991		1.78	3.3E-02	T96545.1	EST_HUMAN	ye49f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
9441	19078		1.59	3.3E-02	M81890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
127	10101	19923	1.13	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1110	11025	20867	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1110	11025	20868	12.7	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1734	11635	21503	1.14	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2072	11962		0.91	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2809	10101	19923	1.15	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
3095	13022	22817	10.71	3.2E-02	BE867353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
3653	13567	23354	1.05	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	14024		12.36	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4658	14544	24333	2.88	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5399	15318	25365	1.46	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
5399	15318	25366	1.46	3.2E-02	X68709.1	NT	S.griseocarneum whiG-Stv gene
5931	15836	25959	2.26	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
5932	15837		26.54	3.2E-02	T89367.1	EST_HUMAN	yd33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains Alu repetitive element;contains LTR1 repetitive element ;
5986	15891	26013	3.72	3.2E-02	AF173845.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
6830	16709	26902	3.48	3.2E-02	6680565	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
7786	17636		3.82	3.2E-02	AA719795.1	EST_HUMAN	zg54b12.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
9952	19487		1.38	3.2E-02	AB021684.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
1239	11146		2.05	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4).mRNA
1283	11191	21043	1.26	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1850	11746	21621	1.35	3.1E-02	6671564	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
1931	11826		1.09	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4152	14052		0.82	3.1E-02	AU119006.1	EST_HUMAN	AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
4767	14652	24440	0.99	3.1E-02	AW835313.1	EST_HUMAN	QV0-LT0014-250200-129-h09 LT0014 Homo sapiens cDNA
6290	16211		2.33	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
7765	17615	27843	2.62	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1606	11511		2.82	3.0E-02	AF187125.1	NT	Pityokteines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
2541	12415	22305	1.07	3.0E-02	AA402242.1	EST_HUMAN	zt65h03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3518	13434	23234	1.07	3.0E-02	M94176.1	NT	Saccharomyces cerevisiae stem-loop mutation supressor SSL2 gene, complete cds
3603	13517	23305	2.61	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3685	13598		0.96	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
3866	13777		1.18	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
4773	14657	24444	0.89	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'
4983	14858	24624	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4983	14858	24625	6.02	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5312	15233		2.88	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6066	16050	26196	2.71	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS gene)
6127	15974	26109	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6127	15974	26110	3.58	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6207	15967	26101	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6207	15967	26102	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
6292	16156	26311	1.54	3.0E-02	M86524.1	NT	Human dystrophin gene
7106	16983		2.11	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
7978	17828	28069	1.71	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
8562	18432	28701	3.09	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8937	18745	29039	7.7	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
9396	19730	24909	1.66	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
9740	19273		4.67	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
9780	19723		2.09	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
2385	12720	22157	1.1	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
2962	12889	22687	1.07	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2962	12889	22688	1.07	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3851	13762	23555	0.92	2.9E-02	H72805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
4950	14827	24593	1.32	2.9E-02	X65137.1	NT	S.vulgare pepC gene for PEP carboxylase
4950	14827	24594	1.32	2.9E-02	X65137.1	NT	S.vulgare pepC gene for PEP carboxylase
5799	15705	25817	6.47	2.9E-02	BF032233.1	EST_HUMAN	601452661F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
6298	16162	26319	10.33	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7568	17419	27635	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
7568	17419	27636	1.94	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
553	10494		0.87	2.8E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3321	13241	23046	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
3321	13241	23047	1.27	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascin (FSCN2) gene, exon 2
4214	14112		0.98	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5373	15293	25140	11.41	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6847	16726	26920	1.33	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9674	19574		1.51	2.8E-02	R06966.1	EST_HUMAN	yf12h02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126675 5'
9680	19237		1.33	2.8E-02	X06322.1	NT	Yeast CN31C *chromosome* III RAHS DNA (*right arm transcription hot-spot*)
1473	11378	21242	1.26	2.7E-02	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3385	13303	23103	2	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4107	14007	23783	2.07	2.7E-02	N47258.1	EST_HUMAN	yy86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4107	14007	23784	2.07	2.7E-02	N47258.1	EST_HUMAN	yy86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'
6205	15965	26099	1.9	2.7E-02	AA993571.1	EST_HUMAN	ot96h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
9648	19500	25134	1.52	2.7E-02	BF514858.1	EST_HUMAN	UI-H-BW1-anj-f-05-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082520 3'
559	10499	20305	1.14	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1345	11251		1.04	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2315	12196	22093	2.9	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.s1 *Stratagene* fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2317	12198	22095	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2317	12198	22096	2.86	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2885	12812		1.55	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
3883	13794		1.13	2.6E-02	AW181945.1	EST_HUMAN	xj68f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2662409 3'
4517	14410		1.13	2.6E-02	BE968922.1	EST_HUMAN	601649877R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933786 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4811	14695	24481	3.69	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
4998	14873	24637	1.67	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5025	14898	24667	2.06	2.6E-02	AW241154.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5771	15678		6.95	2.6E-02	AI206030.1	EST_HUMAN	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
5870	15776	25895	2.08	2.6E-02	BE621748.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6130	15977	26113	6.09	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7388	17306	27512	1.19	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
7948	17798	28038	4.87	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8692	18579		2.1	2.6E-02	AA279351.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
8848	18660	28949	1.89	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BN0-akj-e-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
9320	19715	24906	1.55	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150944 5'
521	10463	20274	1.45	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
521	10463	20275	1.45	2.5E-02	AI793130.1	EST_HUMAN	on26f06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
792	10721	20562	12.83	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
851	10778	20628	4.77	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2735	12597		2.69	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2926	12853	22652	4.4	2.5E-02	X99697.1	NT	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2926	12853	22653	4.4	2.5E-02	X99697.1	NT	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3959	15070	23643	1.09	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
3959	15070	23644	1.09	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4111	14011	23788	5.07	2.5E-02	AW592114.1	EST_HUMAN	hf36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5759	15667		4.48	2.5E-02	BE670128.1	EST_HUMAN	7e30e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.t1 L1 repetitive element ;
5767	15674		3.86	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6519	16378	26555	1.57	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
6519	16378	26556	1.57	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213406 5'
8185	18071	28320	2.45	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
8185	18071	28321	2.45	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
8238	18118	28370	3.38	2.5E-02	AJ237936.1	NT	Bos taurus partial stat5B gene, exons 17-19
8255	18135		3.33	2.5E-02	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li>
8978	18783		1.74	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9280	19657		2.19	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
9463	19528		1.63	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
9581	19167	25271	2.39	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
167	10139	19956	1.01	2.4E-02	AI378582.1	EST_HUMAN	tc72c07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
1580	11484	21344	1.89	2.4E-02	H65884.1	EST_HUMAN	yr75f11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
1998	12710	21784	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1998	12710	21785	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4272	14171	23948	1.4	2.4E-02	J05110.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4420	14314	24099	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4420	14314	24100	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5119	14987		11.51	2.4E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
6962	16840	27032	10.36	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb|K02909|RATSR7K Rat (rRNA);contains A3R.b1 A3R repetitive element ;
7643	17493	27714	2.17	2.4E-02	AV692954.1	EST_HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 5'
7734	17584	27808	2.98	2.4E-02	AA493894.1	EST_HUMAN	nh07b12.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element;contains element PTR5 repetitive element ;
8857	18669	28956	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
8857	18669	28957	1.96	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
9080	18856		1.95	2.4E-02	9627909	NT	Bacteriophage bIL67, complete genome
9224	18947	25357	2.72	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
9282	18984	25326	2.03	2.4E-02	BE928869.1	EST_HUMAN	MR0-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
9368	19036		1.27	2.4E-02	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9506	19120		3.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
9532	19138		1.6	2.4E-02	N42980.1	EST_HUMAN	yy08a06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
9538	19141		1.38	2.4E-02	BF679477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
9977	19667		1.59	2.4E-02	P54643	SWISSPROT	SPORE COAT PROTEIN SP87 PRECURSOR (PL3 PROTEIN)
1829	11726		5.79	2.3E-02	W05340.1	EST_HUMAN	za84g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1844	11740		7.89	2:3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2302	12183	22081	2.52	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3628	13542	23329	4.79	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
4057	13959	23735	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4057	13959	23736	1.19	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4323	14220	24002	1.26	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4347	14244	24027	0.81	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4347	14244	24028	0.81	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4348	15072	24029	0.94	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770671 3'
4348	15072	24030	0.94	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770671 3'
4472	14366	24155	1.75	2.3E-02	BE143160.1	EST_HUMAN	MR0-HT0159-151099-001-e03 HT0159 Homo sapiens cDNA
4490	14384	24171	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4490	14384	24172	2.39	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4948	14825	24591	1	2.3E-02	AI793177.1	EST_HUMAN	qz35c03.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
4948	14825	24592	1	2.3E-02	AI793177.1	EST_HUMAN	qz35c03.x5 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028868 3'
5302	16223	26027	3.57	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
5990	15895	26018	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6598	16478	26665	5.67	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7764	17614	27841	1.51	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7764	17614	27842	1.51	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
8162	18050	28302	2.15	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9201	19512		4.41	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
9713	19254	25219	1.94	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
9767	19756		2.27	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
9961	19609		1.27	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
720	10652	20482	3.09	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1713	11614		1.53	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1968	11861	21752	1.78	2.2E-02	Z82001.1	NT	S.pneumoniae pcpA gene and open reading frames
2695	12730	22448	1.4	2.2E-02	AF109633.1	NT	Mus musculus ets variant protein ER81 gene, exons 1 through 4
3388	13306		1.93	2.2E-02	AA577785.1	EST_HUMAN	nn24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3595	13509		3.27	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3779	13691	23477	1.05	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3844	13755	23549	0.99	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
6297	16161	26318	3.78	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
6876	16755	26952	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
6876	16755	26953	2.26	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7585	17436	27651	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7585	17436	27652	2.33	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9466	19096		2.24	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;
413	10359		5.56	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
441	10385		7.99	2.1E-02	AF029726.1	NT	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds
1242	11149	20998	7.43	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CotL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1365	11270	21125	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1365	11270	21126	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1920	11815	21694	0.95	2.1E-02	AF190899.1	NT	Tegula aureotincta major acrosomal protein precursor (TMAP) mRNA, complete cds
2785	10693	20530	3.98	2.1E-02	N29266.1	EST_HUMAN	yx43h07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264541 5'
3110	11883	21776	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3110	11883	21777	0.85	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3536	13451	23247	1.23	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796121 5'
4038	13941	23719	0.89	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4342	14239	24022	1.61	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4351	14247	24033	1.03	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4611	14499	24288	4.65	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4714	14600	24386	0.86	2.1E-02	AI823432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
7553	17404	27618	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7553	17404	27619	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9449	15095		4.99	2.1E-02	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
9857	19348	25184	3.33	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds
17	10004	19795	1.35	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element ;
18	10005	19796	7.86	2.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
259	10225	20040	2.63	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
292	10256	20077	2.62	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
781	10711	20550	1.75	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1071	10987	20830	0.97	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1[1p36.33] of Homo sapiens
1181	11092	20938	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1181	11092	20939	1.61	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1830	11727	21600	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1830	11727	21601	2.31	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2768	12630		1.75	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3040	10004	19795	1.96	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.t3 MER1 repetitive element ;
3105	13031		1.16	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3189	13114		3.33	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3925	13834	23614	1.5	2.0E-02	M18095.1	NT	P.vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5079	14949	24725	0.99	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5085	14955	24730	0.99	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
7679	17529		1.8	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7930	17780	28019	1.59	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
8037	17929	28175	2.01	2.0E-02	Z73966.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
8678	18566	28849	2.55	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
8931	18739	29031	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
8931	18739	29032	3.09	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
9019	14955	24730	1.41	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
9481	12630		1.56	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9928	19536		1.72	2.0E-02	BE786595.1	EST_HUMAN	601478819F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881477 5'
9935	19404		4.08	2.0E-02	T80037.1	EST_HUMAN	yd04c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24675 5'
678	10611	20432	1.68	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.t1 L1 repetitive element ;
1599	11504	21364	0.84	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
1993	11887	21779	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1993	11887	21780	2.52	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2458	12335	22230	0.87	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2875	12802	22596	7.08	1.9E-02	AA713856.1	EST_HUMAN	nw04f05.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2923	12850	22650	1.53	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3222	13146		0.82	1.9E-02	AB033611.1	NT	Urotrichus talpoides mitochondrial gene for cytochrome b, complete cds
3560	13474		1.25	1.9E-02	N52250.1	EST_HUMAN	yz28b02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284331 3'
3644	13558		5.75	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
3654	13568	23355	0.98	1.9E-02	AI301183.1	EST_HUMAN	qn04c07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;
3961	13868	23646	1.14	1.9E-02	AF141940.1	NT	Mycoplasma imitans VlhA1 precursor (vlhA1) and VlhA2 precursor (vlhA2) genes, partial cds
4099	13999	23777	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	13999	23778	1.47	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4441	14335	24125	2.51	1.9E-02	AI452999.1	EST_HUMAN	tj46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
4944	12335	22230	1.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5356	15276	25106	1.29	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
6985	16862		1.29	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
7377	17246	27452	1.47	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
7777	17627	27859	1.31	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
9234	19516	25137	2.55	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gliarin mRNA, complete cds
343	10302	20117	1.44	1.8E-02	AW771104.1	EST_HUMAN	hn52c06.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element ;
670	10604	20421	1.14	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1144	11057	20900	1.34	1.8E-02	X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1417	11323	21187	1.23	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2645	12512	22403	1.51	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3174	13099		0.89	1.8E-02	AI805829.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3812	13724	23513	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3812	13724	23514	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3996	13903		1.15	1.8E-02	AA861446.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4332	14229	24011	1.44	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
4873	14753	24532	1.05	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.2
4887	14767	24543	1.06	1.8E-02	AI288701.1	EST_HUMAN	qm06b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881007 3'
6075	16058	26207	3.96	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7560	17411		2.49	1.8E-02	AA897543.1	EST_HUMAN	aj62f09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb:L11672 ZINC FINGER PROTEIN 91 (HUMAN);

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7790	17640	27873	1.51	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
7871	17721	27966	1.23	1.8E-02	X96933.1	NT	L.stagnalis mRNA for myomodulin neuropeptide precursor
8735	17884	28126	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8735	17884	28127	1.78	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8886	18697	28991	1.76	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7)
8897	18706	29000	3.12	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
9912	19496		1.29	1.8E-02	AF047475.1	NT	Drosophila melanogaster projectin (projectin) gene, partial cds
888	10814	20662	1.29	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1750	11650	21519	2.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;
1750	11650	21520	2.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;
1828	11725		3.08	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2066	11956		13.03	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2603	12471		1.35	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2968	12895	22695	0.92	1.7E-02	AI147616.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3467	13383		4.17	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element ;
3573	13487		0.88	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4078	13980		0.98	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element;contains element MER24 repetitive element ;
4105	14005		1.78	1.7E-02	R02506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4427	14322	24109	1.24	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.t1 L1 repetitive element ;
4615	14503	24291	1.77	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4708	14594		5.27	1.7E-02	AI015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
4967	14842	24612	5.47	1.7E-02	AF105037.1	NT	Murid herpesvirus 4 complete genome
5725	15632	25735	1.53	1.7E-02	AI769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6276	16140	26296	2.31	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
6554	16412		1.81	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7592	17443	27659	1.48	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434I0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0314 5'
9781	19683	24995	2.25	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-f06 NN1030 Homo sapiens cDNA
9861	19352		1.96	1.7E-02	Q03211	SWISSPROT	PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
501	10443		1.58	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1635	11539	21399	1.13	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2202	12089	21990	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2202	12089	21991	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2518	12392	22284	0.98	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2606	12474	22368	1.47	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2662	12529		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3481	13397	23202	3.83	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
4084	13986		2.16	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4203	14102	23885	0.94	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-f07 PT0012 Homo sapiens cDNA
5456	15377	25437	1.31	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6003	15908	26032	2.11	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
6758	16637		4.01	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
7773	17623		2.71	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
7954	17804	28044	1.47	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1] ;
7954	17804	28045	1.47	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT P29294 TELOKIN. [1] ;
8280	19473	28401	2.17	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEI0260 (=T16iiiE11))
8544	18416	28683	2.52	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8544	18416	28684	2.52	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8801	18615	28905	1.91	1.6E-02	AI373558.1	EST_HUMAN	qz96e10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
9211	12089	21990	1.35	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9211	12089	21991	1.35	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
9577	19165		2.3	1.6E-02	X92751.1	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)
9973	19433		1.42	1.6E-02	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
734	10666		24.9	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2095	11984	21879	3.81	1.5E-02	N39521.1	EST_HUMAN	yv27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925 3'
2128	12016	21914	2.38	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3023	12951	22743	1.44	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3023	12951	22744	1.44	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3663	13577	23365	0.9	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4049	13951	23727	1.23	1.5E-02	AA160967.1	EST_HUMAN	zq40g10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632226 5'
4367	14263	24048	0.91	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5801	15707	25819	1.91	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
6332	16195		1.66	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
6377	16239	26399	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
6596	16476	26664	1.53	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6600	16480	26668	3.44	1.5E-02	11417739	NT	Homo sapiens valyl-tRNA synthetase 2 (VARS2), mRNA
7126	17003	27195	1.23	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'
7520	17339	27545	2.07	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GepC
7646	17496	27717	1.26	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
7646	17496	27718	1.26	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
8508	18380	28647	2.5	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
9429	19559		1.32	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
9980	19437		1.47	1.5E-02	AU134730.1	EST_HUMAN	AU134730 PLACE1 Homo sapiens cDNA clone PLACE1000374 5'
411	10357		1.45	1.4E-02	AE002230.2	NT	Chlamydophila pneumoniae AR39, section 58 of 94 of the complete genome
1102	11018	20860	3.58	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1236	11143		1.35	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1276	11184		2.82	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1374	11280		0.94	1.4E-02	AF216854.1	NT	Homo sapiens headpin gene, complete cds
1501	11405		0.96	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3176	13101	22805	1.9	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xylR) gene, partial cds
3352	13272	23074	0.99	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3439	13356	23161	5.21	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3439	13356	23162	5.21	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3476	13392	23197	0.98	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3606	13520	23308	6.16	1.4E-02	6996918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4387	14283	24062	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4387	14283	24063	7.29	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGG Homo sapiens cDNA
4775	14659	24445	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4775	14659	24446	6.7	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5862	15768	25887	4.62	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
5862	15768	25888	4.62	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6732	16612		1.82	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
7408	17275	27481	2.07	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
9126	18885	28790	4.79	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
9476	19102		1.55	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
9763	19277		1.89	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1821	11718		0.86	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
1912	11807	21684	2.41	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22906	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3177	13102	22907	1.99	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3888	13799		1.41	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5176	11807	21684	1	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5212	15135	24854	1.36	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5212	15135	24855	1.36	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6156	15114	24856	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6156	15114	24857	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6473	16332	26499	4.77	1.3E-02	AI031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
6939	16817	27010	1.74	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7862	17712	27956	1.87	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
8360	18237	28484	4.39	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
8360	18237	28485	4.39	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
9102	19705		2.92	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
9482	19694		1.6	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
9586	19170		1.8	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
9758	19486		28.84	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
9949	19744	24912	1.32	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds
206	10177		0.94	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
352	10310	20128	1.74	1.2E-02	AA059299.1	EST_HUMAN	zf65g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element ;
445	10389	20210	1.48	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
721	10653	20483	2.98	1.2E-02	AI183522.1	EST_HUMAN	qd68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element ;
2130	12018	21916	1.99	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2393	12271	22167	1.23	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2448	12325	22223	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068408F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2448	12325	22224	1.1	1.2E-02	BE538310.1	EST_HUMAN	601068408F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2596	12271	22167	1.27	1.2E-02	AW172350.1	EST_HUMAN	xj37e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3063	12990		6.18	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3250	13173	22971	1.89	1.2E-02	R62805.1	EST_HUMAN	yi11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4830	14712	24495	2.04	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4974	14849		1.73	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiqT mRNA, partial cds
5017	14891	24659	2.12	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5516	15434	25497	1.96	1.2E-02	D78589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6180	16066	26216	5.33	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6327	16190	26352	6.37	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
6665	16545	26742	2.11	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
6765	16644	26832	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
6765	16644	26833	1.22	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
7152	17029		1.17	1.2E-02	T76987.1	EST_HUMAN	yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'
7557	17408	27623	2.45	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
7575	17426	27640	1.23	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
9177	18918	25345	1.78	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGUI) (HPER)
9588	19575		1.5	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
9766	19286		3.47	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-557G06 5'
1248	11155	21004	1.32	1.1E-02	AA070364.1	EST_HUMAN	zm69e11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1679	11581	21451	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1679	11581	21452	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4

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Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1992	11886	21778	4.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2848	12776		3.53	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
2933	12860	22660	10.39	1.1E-02	AF055066.1	NT	Homo sapiens MHC class 1 region
3478	13394	23200	2.46	1.1E-02	AI653508.1	EST_HUMAN	tq95b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPF_HUMAN Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
3937	13846		0.87	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-300999-001-h06 HT0175 Homo sapiens cDNA
4016	13921		0.97	1.1E-02	AW813796.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4723	14609	24395	1.81	1.1E-02	AL048383.2	EST_HUMAN	DKFZp586E0924_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
4821	14704		0.92	1.1E-02	AW820281.1	EST_HUMAN	QV2-ST0296-150200-028-c11 ST0296 Homo sapiens cDNA
6480	16339	26506	2.26	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
7160	17037	27230	6.87	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7710	17560	27785	2.25	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
7810	17660	27900	4.1	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
8347	18224	28476	3.38	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
9064	18845		2.23	1.1E-02	AA668239.1	EST_HUMAN	ab77f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains Alu repetitive element;
6	9992	19785	3.35	1.0E-02	AW846120.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
1506	11411	21270	0.91	1.0E-02	AW368128.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
2525	12399		1.2	1.0E-02	AA806389.1	EST_HUMAN	oc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3051	12978	22771	2.37	1.0E-02	BE835556.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
3226	13150	22950	1.18	1.0E-02	BE968999.1	EST_HUMAN	601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3464	13380		0.99	1.0E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
3805	13717	23505	0.79	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4667	14553	24345	4.26	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Crhr2), mRNA
4736	14621	24407	2.38	1.0E-02	R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199633 5'
4995	14870	24633	0.85	1.0E-02	AF218910.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
5149	15016		0.82	1.0E-02	BE876539.1	EST_HUMAN	601486286F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888908 5'
5751	15659	25766	2.74	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
5751	15659	25767	2.74	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6054	16037	26178	2.06	1.0E-02	Z29642.1	NT	Z.mays U3snRNA pseudogene
7403	17270	27475	4.65	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
7403	17270	27476	4.65	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8586	18454		2.1	1.0E-02	AF157559.1	NT	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
8674	18562	28846	2.03	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
9142	19762		1.7	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
9202	19535	25061	2.95	1.0E-02	AW935521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
9217	19590		5.22	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
9745	19645		2.44	1.0E-02	X62654.1	NT	H.sapiens gene for Me491/CD63 antigen
875	10801	20651	1.7	9.0E-03	AI796126.1	EST_HUMAN	wh42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element ;
1243	11150		1.97	9.0E-03	BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2346	12226	22123	3.26	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2593	12463	22355	1.08	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2593	12463	22356	1.08	9.0E-03	AJ243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12803	22597	0.83	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2876	12803	22598	0.83	9.0E-03	AI251744.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3617	13531	23317	0.92	9.0E-03	J05184.1	NT	S.acidocaldarius thermopsin gene, complete cds
4914	14793	24568	1.17	9.0E-03	BE047949.1	EST_HUMAN	tz44e10.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291466 5'
5181	15045		2.56	9.0E-03	AF137240.1	NT	Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds
5997	15902		4.17	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
6597	16477		1.18	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
7673	17523	27749	1.47	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
8354	18231		1.95	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
9352	19763		1.34	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
9557	19768		11.59	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
9562	15045		1.27	9.0E-03	AF137240.1	NT	Sargocentron sp. mixed lineage leukemia-like protein (Mll) gene, partial cds
9649	19215	25259	1.62	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
9843	19341		27.64	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291299-001-e09 HT0452 Homo sapiens cDNA
493	10436		3.2	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains Alu repetitive element;
973	10897	20744	45.2	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2113	12002	21900	2.38	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2930	12857		0.86	8.0E-03	U47048.1	NT	Escherichia coli microcin 24 region, DNA binding protein (mdbA), immunity protein (mtfI), microcin 24 (mtfS), and microcin transport protein (mtfA, mtfB) genes, complete cds
3270	13191	22890	0.97	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3314	13235	23039	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3792	13704		1.07	8.0E-03	AF058764.1	NT	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
4286	14185	23966	5.12	8.0E-03	BF363327.1	EST_HUMAN	CM4-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5391	15310	25164	2.7	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5761	19453	25775	1.35	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position (2/7)
6048	15951	26081	4.52	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6279	16143	26299	2.19	8.0E-03	M17197.1	NT	A.californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end
6453	16314		1.86	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7166	17043	27235	3.81	8.0E-03	AW808692.1	EST_HUMAN	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
7717	17567		4.72	8.0E-03	BE086509.1	EST_HUMAN	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
8148	18036	28284	1.92	8.0E-03	BE788441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
8353	18230		2.78	8.0E-03	Z49652.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
8687	18575	28858	1.75	8.0E-03	AA828817.1	EST_HUMAN	od80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8687	18575	28859	1.75	8.0E-03	AA828817.1	EST_HUMAN	od80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8953	18760	29053	4.83	8.0E-03	AF064689.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
9075	18852		1.34	8.0E-03	M69035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
9121	18882		3.36	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
679	10612	20433	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20434	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
961	10884	20732	2.01	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1100	11016	20858	2.6	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1341	11247		1.19	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1373	11279	21135	13.73	7.0E-03	AA668298.1	EST_HUMAN	ab79b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
1486	11391	21251	4.6	7.0E-03	AW303599.1	EST_HUMAN	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2210	12715	22001	2.24	7.0E-03	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3702	13616	23400	1.27	7.0E-03	AW444463.1	EST_HUMAN	UI-H-BI3-akb-c-10-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3741	13653	23436	1.01	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4434	14329		1.23	7.0E-03	AW117711.1	EST_HUMAN	xe34f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR:Q12987 Q12987 ACIDIC 82 KDA PROTEIN. ;
4495	14389		1.01	7.0E-03	AW630888.1	EST_HUMAN	hh89a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969936 5'
4916	14795		1.76	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5038	14910	24683	1.1	7.0E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434 O93434 RETICULOCALBIN. ;
5038	14910	24684	1.1	7.0E-03	BE044191.1	EST_HUMAN	ho39h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:O93434 O93434 RETICULOCALBIN. ;
5717	19452		5.07	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
5813	15718	25831	1.49	7.0E-03	W68251.1	EST_HUMAN	zd33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
5939	15844	25967	3.46	7.0E-03	AA327129.1	EST_HUMAN	EST30674 Colon I Homo sapiens cDNA 5' end
5954	15859	25980	1.3	7.0E-03	BE857385.1	EST_HUMAN	7g34b10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387 Q13387 HYPOTHETICAL PROTEIN 384D8_2. ;contains TAR1.t2 TAR1 TAR1 repetitive element ;
6210	15992	26127	2.39	7.0E-03	BE928133.1	EST_HUMAN	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
6441	16302	26466	4.98	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
6441	16302	26467	4.98	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
6723	16603	26792	2.29	7.0E-03	BE175667.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
7605	17456	27670	2.53	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7605	17456	27671	2.53	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7906	17756		1.27	7.0E-03	AV687379.1	EST_HUMAN	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
8201	18086	28337	3.36	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
9609	19750		1.55	7.0E-03	H94065.1	EST_HUMAN	yv15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains Alu repetitive element;
9615	19194		1.88	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
9962	19425		1.83	7.0E-03	AW868110.1	EST_HUMAN	RC0-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
1220	11129	20979	9.29	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
1220	11129	20980	9.29	6.0E-03	AW511148.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O75469 ORPHAN NUCLEAR RECEPTOR PXR ;
2744	12606	22499	1.09	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2862	12790	22581	3.11	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
2862	12790	22582	3.11	6.0E-03	AA759135.1	EST_HUMAN	ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3208	13132		2.06	6.0E-03	H75690.1	EST_HUMAN	yr77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3264	13187		0.82	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13256	23062	1.24	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3336	13256	23063	1.24	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3499	13416		1.05	6.0E-03	W37985.1	EST_HUMAN	zc13a11.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3610	13524	23311	3.62	6.0E-03	BF510986.1	EST_HUMAN	UI-H-BI4-apm-c-06-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3711	13624	23407	1.28	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
3846	13757	23551	0.93	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
3873	13784		1.18	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959513 5'
4231	14129		0.87	6.0E-03	N58946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278179 3'
4267	14166		1.37	6.0E-03	AI016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4597	14485	24271	6.82	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5115	14983	24758	1.83	6.0E-03	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5129	14996	24767	0.89	6.0E-03	AA889972.1	EST_HUMAN	aj95g09.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404256 3'
6506	16365	26542	1.97	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
6586	16466	26657	7.04	6.0E-03	AI033980.1	EST_HUMAN	ow13a04.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element ;
6650	16530	26724	2.44	6.0E-03	AW799337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
6689	16569		1.41	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858626 5'
7509	17297	27506	8.21	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7776	17626		1.94	6.0E-03	AI432661.1	EST_HUMAN	ti22c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
7949	17799	28039	1.5	6.0E-03	X68366.1	NT	M.thermoformicicum complete plasmid pFV1 DNA
8127	18015	28263	2.23	6.0E-03	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
8186	18072		2.21	6.0E-03	11545814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
8220	18102	28356	1.89	6.0E-03	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
8220	18102	28357	1.89	6.0E-03	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
8350	18227		3.91	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
8351	18228	28479	3.54	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9185	18922		1.59	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 148) of the complete genome
9372	19038		1.34	6.0E-03	AB025356.1	NT	Anguilla japonica mRNA for activin B, complete cds
9392	19583		2.21	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9722	19262		1.57	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
9741	19274		1.34	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
653	10589	20406	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
653	10589	20407	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20406	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
654	10589	20407	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1096	11012	20854	1.38	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase,RH3
1552	11457		0.91	5.0E-03	AI138977.1	EST_HUMAN	qd79d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2648	12515	22405	3.44	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2905	12832	22629	0.95	5.0E-03	BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3097	13024	22820	4.08	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3116	13041		1.75	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3129	13054	22853	1.04	5.0E-03	R71794.1	EST_HUMAN	yj86g02.s1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:155666 3'
3240	13163		1.08	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3641	13555	23341	4.16	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3698	13612	23396	0.83	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3890	13801		1.38	5.0E-03	AA299675.1	EST_HUMAN	EST12218 Uterus tumor I Homo sapiens cDNA 5' end
4207	14106	23886	0.93	5.0E-03	H78355.1	EST_HUMAN	yu79g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240066 5'
4209	13612	23396	0.91	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4503	14396	24181	0.94	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4619	14507	24296	2.49	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5541	15458	25528	5.34	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5685	15594	25695	2.43	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5977	15881		6.17	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6091	15101	24877	6.02	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6566	16424	26605	6.26	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
6794	16673	26865	1.97	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7006	16883		6.92	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8103	17993		7.44	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
8310	18187	28435	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.t2 L1 repetitive element ;
8310	18187	28436	3.17	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1.t2 L1 repetitive element ;
8399	18275	28527	1.95	5.0E-03	T49153.1	EST_HUMAN	yb09e04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
8433	18307	28563	1.77	5.0E-03	10946753	NT	Mus musculus hypothetical protein, MNCb-4760 (LOC58212), mRNA
8644	18508		3.73	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291622 5'
9327	19709		5.04	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
9460	19091		8.65	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
9555	19153		1.55	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
9592	19174		1.28	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT ;
9616	19529		4.16	5.0E-03	BF572332.1	EST_HUMAN	602077774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9791	19301	25197	1.94	5.0E-03	AW449109.1	EST_HUMAN	UI-H-BI3-akf-f-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
9808	19601		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
9929	19400		1.41	5.0E-03	AI668709.1	EST_HUMAN	zb74g05.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:309368 3'
232	10201	20015	2.97	4.0E-03	AW500196.1	EST_HUMAN	UI-HF-BN0-akc-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
318	10280	20097	2.18	4.0E-03	R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
436	10380	20203	0.94	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
588	10526	20333	3	4.0E-03	AA939339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
859	10785	20637	1.81	4.0E-03	R46482.1	EST_HUMAN	yg51e04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
893	10819		3.43	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
1133	11047	20889	32.55	4.0E-03	AA099777.1	EST_HUMAN	zl81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1153	11066	20910	1.68	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1281	11189	21040	1.33	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1568	11472		1.31	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1709	11610	21480	2.2	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
1971	11864	21757	20.87	4.0E-03	AA099777.1	EST_HUMAN	zl81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2200	12087		1.66	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2232	12117	22019	1.46	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2526	12400	22290	1.89	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2526	12400	22291	1.89	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2659	12526	22414	2.86	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2659	12526	22415	2.86	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2664	12530	22418	1.02	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3487	13403	23207	0.94	4.0E-03	AW188426.1	EST_HUMAN	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3487	13403	23208	0.94	4.0E-03	AW188426.1	EST_HUMAN	xj98f04.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3572	13486	23278	0.8	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 5I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3836	13486	23278	0.83	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 5I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3852	13763	23556	0.85	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
3914	13823		1.79	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4509	14402	24190	1.13	4.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
5164	15030	24796	13.17	4.0E-03	J02187.1	NT	Foot and mouth disease virus serotype A-12 119ab capsid protein VP3
5225	15149	24916	1.66	4.0E-03	AF005859.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5315	15236	25039	19.53	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5540	15457	25527	4.23	4.0E-03	P04196	SWISSPROT	(HPRG)
5542	15459	25529	1.5	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
5704	15612		3.23	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5809	15714	25827	1.76	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6062	16045	26190	1.52	4.0E-03	U76408.1	NT	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete cds
6271	16136	26291	4.14	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6690	16570	26762	3.61	4.0E-03	AF111944.1	NT	Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6774	16653	26841	2.02	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7056	16933	27123	7.4	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element;
7151	17028		4.41	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7159	17036	27229	3.38	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8472	18345	28609	5.64	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9295	19725		3.95	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
9317	19009		2.25	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
9628	19202		3	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element;contains element MER31 repetitive element ;
9666	19640		1.57	4.0E-03	AW614596.1	EST_HUMAN	hh02c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element ;
9679	19236		1.57	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
9950	19416	26168	1.52	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
367	10323	20146	1.62	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
861	10787	20638	7.66	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1638	11542	21401	1.84	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2211	12097		0.87	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2248	12132		3.9	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2249	12133	22029	1.12	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2249	12133	22030	1.12	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2963	12890		0.84	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoMt gene
3044	12971	22765	4.53	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3112	13037	22833	2.62	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3371	13290	23089	1.95	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3379	13297		6.75	3.0E-03	Y12500.1	NT	C.elegans samdc gene
3895	13805	23591	7.43	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3895	13805	23592	7.43	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
3950	13858	23632	1.58	3.0E-03	AI792278.1	EST_HUMAN	ah04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4058	13960		1.34	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
4296	14194	23978	11.91	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4417	14311	24096	4.37	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4630	14518	24309	0.88	3.0E-03	AL119067.1	EST_HUMAN	DKFZp761B0712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4727	14613	24399	1.54	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x5 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4745	14630	24416	7.09	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5089	14959	24733	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5089	14959	24734	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5220	15143	24837	3.17	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5410	15330	25380	1.41	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5946	15851	25974	9.97	3.0E-03	AA456701.1	EST_HUMAN	aa13f10.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6277	16141	26297	1.54	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcpl3 gene for purine-cytosine permease
6442	16303	26468	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
6741	16620	26809	2.01	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
6928	16806	27001	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
6940	16818	27011	1.57	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6991	16868		1.38	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
7199	17076		8.52	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969131 3' similar to contains L1.t1 L1 repetitive element ;
7230	17107	27297	4.1	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
7244	17121	27317	8.9	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rna1 HISTONE H2B.2 (HUMAN);
7598	17449		3.48	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7694	17544	27768	1.29	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
7742	17592	27813	1.46	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
7836	17686	27931	4.05	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8222	18104		2.69	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
8685	18573	28856	2.11	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
8744	17893	28137	2.01	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
8773	18590	28877	3.06	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8773	18590	28878	3.06	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8841	18654	28942	1.93	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9068	19542		2.02	3.0E-03	AI525056.1	EST_HUMAN	promrna-5.E07.r bvtumor Homo sapiens cDNA 5'
9103	18870	28780	1.54	3.0E-03	AA993154.1	EST_HUMAN	ot77b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.t3 MER26 repetitive element ;

Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9159	19668		1.35	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
9339	19019	25296	2.33	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
504	10446	20258	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
504	10446	20259	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
768	12677		7.01	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1340	11246	21104	1.93	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1343	11249	21106	1.59	2.0E-03	AA661605.1	EST_HUMAN	nu86f01.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217593
1353	11259	21115	12.6	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1474	11379	21243	1.11	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1500	11404	21263	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1500	11404	21264	1.91	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1573	11477		4.94	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1733	11634	21502	1.38	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1950	11845	21731	2.17	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2203	12090	21992	1.04	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2535	12409		4.62	2.0E-03	AW137782.1	EST_HUMAN	UI-H-BI1-adi-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3370	13289	23088	4.03	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3376	13294	23093	1.02	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3615	13529	23315	4.87	2.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
3869	13780	23572	0.92	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4024	13927	23703	2.16	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4127	14027		9.77	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4446	14340	24130	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4446	14340	24131	1.93	2.0E-03	L42512.1	NT	Drosophila melanogaster shortsighted class 2 (shs) mRNA, complete cds
4608	14498	24285	0.94	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4612	14500		1.7	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
5077	14947		0.82	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
5194	15057	24820	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
5194	15057	24821	1.04	2.0E-03	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5372	15292	25128	1.37	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5457	19445	25438	1.76	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5501	15420	25482	1.87	2.0E-03	U63711.1	NT	Xenopus laevis xefiltin mRNA, complete cds
5716	15624	25725	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5716	15624	25726	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5829	15735	25846	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5829	15735	25847	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5831	15737	25849	7.14	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5850	15756	25874	2.2	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5861	15767	25886	1.95	2.0E-03	X94451.1	NT	L.esculentum mRNA for lysyl-tRNA synthetase (LysRS)
5979	15884		1.36	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
6212	15994	26129	2.88	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0366-061299-054-d01 BT0366 Homo sapiens cDNA
6691	16571	26763	2.11	2.0E-03	AW592004.1	EST_HUMAN	hf37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60976 Q60976 JERKY. ;
6784	16663	26853	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
6784	16663	26854	5.19	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
7513	17301	27508	3.12	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
7775	17625		5.41	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
8379	18256		2.78	2.0E-03	M86524.1	NT	Human dystrophin gene
8779	16350	26520	1.78	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8829	18642		1.77	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
8836	18649	28936	12.17	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
9052	18835		2.07	2.0E-03	AI625745.1	EST_HUMAN	ty65h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
9066	18847	29115	2.88	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
9113	14947		4.48	2.0E-03	AJ245167.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
9322	19703		2.76	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9414	19066	25278	1.59	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
9455	19087		9.62	2.0E-03	D84278.1	NT	Human DNA for CD38, exon 1
9525	19134		2.92	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9582	19569		1.67	2.0E-03	AI375037.1	EST_HUMAN	te66f02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;
9696	19247		1.27	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9856	19521		1.66	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
432	10377	20198	1.38	1.0E-03	H96471.1	EST_HUMAN	yt98c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
812	10740	20587	2.38	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
812	10740	20588	2.38	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1079	10995	20836	2.14	1.0E-03	AI865788.1	EST_HUMAN	wk86a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1099	11015	20857	1.44	1.0E-03	AI954572.1	EST_HUMAN	wx93e10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1150	11063	20906	1.45	1.0E-03	AI692616.1	EST_HUMAN	wd86a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1982	11875	21768	3.61	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2108	11997	21896	8.02	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2951	12878	22676	1.15	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3154	13079	22879	2.26	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3154	13079	22880	2.26	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3262	13185	22984	1.16	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3496	13413	23218	0.79	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3496	13413	23219	0.79	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3614	13528		1.24	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3855	13766	23559	1.02	1.0E-03	Z49649.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4334	14231	24013	3.54	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4377	14273	24054	3.77	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4564	14456	24244	0.87	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4717	14603	24388	1.78	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4717	14603	24389	1.78	1.0E-03	AI073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4718	14604		6.23	1.0E-03	BE154067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5009	14883	24649	16.98	1.0E-03	O46409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5103	14971	24747	0.93	1.0E-03	AV685870.1	EST_HUMAN	AV685870 GKC Homo sapiens cDNA clone GKCDME11 5'
5250	15173	24946	2.03	1.0E-03	AA290951.1	EST_HUMAN	zs44f01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5317	15238	25042	3.06	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5349	15269	25096	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5349	15269	25097	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5423	15344	25397	1.69	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5666	15577		4.08	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5758	15666		8.56	1.0E-03	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
5824	15730	25842	1.32	1.0E-03	T87761.1	EST_HUMAN	yd93a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115772 5'
5857	15763		1.4	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6242	16108	26259	2.4	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
6419	16281		1.37	1.0E-03	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
6503	16362	26537	1.63	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
6536	16394	26573	3.13	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
6636	16516	26707	5.35	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6798	16677	26867	2.39	1.0E-03	AF153980.1	NT	Homo sapiens exostoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
7175	17052		1.4	1.0E-03	Y11204.1	NT	V.carteri gene encoding volvoxopsin
7273	17150	27345	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7273	17150	27346	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
7541	17392	27602	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
7541	17392	27603	1.85	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
8056	17947	28196	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8056	17947	28197	22.37	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-a09 CT0279 Homo sapiens cDNA
8133	18021	28268	2.44	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
8198	18083		2.69	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE. ;
8497	18370		3.4	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
9046	18831	29113	2.82	1.0E-03	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9491	19108	25287	1.95	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
9517	19687		2.15	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
9626	19707	24904	4.2	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5131	14998	24769	0.81	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5485	15404		1.56	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
7561	17412		1.42	9.0E-04	AB037203.1	NT	Glycyrrhiza glabra GgbAS1 mRNA for beta-amyrin synthase, complete cds
1472	11377		1.39	8.0E-04	X96469.1	NT	X.laevis mRNA for C4SR protein
3843	13754	23548	1.27	8.0E-04	R07008.1	EST_HUMAN	yf12h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126691 5'
4089	13989		4.2	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4656	14542	24332	2.39	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
8485	18358		2.08	8.0E-04	AA777084.1	EST_HUMAN	zf24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
8616	18483		2.16	8.0E-04	AI571099.1	EST_HUMAN	tn85a08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2176310 3'
1786	11684	21562	1.61	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2350	12230	22127	1.13	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2682	12547	22437	3.26	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3243	13166	22965	1.03	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
5923	15828		2.24	7.0E-04	AI769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
8851	18663		3.2	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8871	18683	28973	2.61	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
9558	19155		3.29	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
9790	19300		2.72	7.0E-04	R17336.1	EST_HUMAN	yg13c06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
9813	19321		3.28	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
3877	13788	23576	1.34	6.0E-04	AI862525.1	EST_HUMAN	wj15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
3999	13905	23680	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
3999	13905	23681	0.85	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4092	13992	23769	3.28	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6590	16470		4.35	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7733	17583		3.13	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
7800	17650	27887	2.24	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
8776	18593	28881	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8852	18664	28950	6.32	6.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
8906	18714		2.45	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9225	19598		2.26	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0269-261199-012-d08 HT0269 Homo sapiens cDNA
9958	19421	25170	1.49	6.0E-04	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
635	10572	20385	5.82	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF92)
1485	11390		1.83	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3367	13286	23085	1.42	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
5361	15281	25113	2.19	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5996	15901	26026	5.72	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
6364	16227	26387	13.6	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
6639	16519	26710	5.57	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN);contains Alu repetitive element;
7345	17213	27412	1.45	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
7543	17394	27606	4.69	5.0E-04	AW270938.1	EST_HUMAN	xs06e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
8343	18220		4.17	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
8950	15281	25113	17.6	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9164	19530		2.27	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913875
9944	19413		1.46	5.0E-04	AW241666.1	EST_HUMAN	xm77h09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2690273 3'
386	10333		1.13	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
657	10592	20410	1.42	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
829	10756	20606	1.57	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
829	10756	20607	1.57	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1449	11354	21218	3.92	4.0E-04	AW763356.1	EST_HUMAN	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2037	11928	21823	1.68	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2086	11976		1.19	4.0E-04	AL046704.1	EST_HUMAN	DKFZp434D059_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'
2586	12457	22348	2.73	4.0E-04	O96615	SWISSPROT	SERICIN-2 (SILK GUM PROTEIN 2)
3127	13052	22850	1.89	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3316	13237	23041	0.84	4.0E-04	AV696624.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFFH07 5'
4228	14126	23900	2.75	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4228	14126	23901	2.75	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4437	14332	24121	1.28	4.0E-04	AA086324.1	EST_HUMAN	zn61c08.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
5020	14893	24661	3.72	4.0E-04	BE560660.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5132	14999	24770	0.9	4.0E-04	N48313.1	EST_HUMAN	yy78b10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279643 3' similar to contains Alu repetitive element;
6972	16849	27040	1.62	4.0E-04	N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264142 5'
7588	17439	27655	2.79	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
7662	17512		1.44	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
9526	19505		1.52	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
9677	19479		1.84	4.0E-04	Q05860	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)
150	10124	19942	3.04	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
188	10160	19977	2.22	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
862	10788	20639	1.27	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1810	11707		1.16	3.0E-04	AI399674.1	EST_HUMAN	th23a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2119082 3'
3268	13180	22988	3.37	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3882	13793	23581	3.63	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3969	13876		1.18	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4711	14597		4.5	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4784	14669	24456	0.85	3.0E-04	AW937723.1	EST_HUMAN	QV3-DT0045-221299-046-d09 DT0045 Homo sapiens cDNA
6052	14924		1.34	3.0E-04	Y11204.1	NT	V.carteri gene encoding volvoxopsin
5735	15643		4.82	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6081	16026	26166	5.88	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6806	16685	26875	3.49	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
7705	17555	27780	1.42	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
7977	17827	28068	3.66	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391288 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
9118	19726	24908	2.33	3.0E-04	AA228301.1	EST_HUMAN	nc38e04.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.t2 L1 repetitive element ;
9483	19576	25068	4.32	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
9874	19361		2.01	3.0E-04	AL134483.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547L185 5'
169	10141	19957	1.18	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
470	10413	20232	2.15	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
889	10815	20663	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
889	10815	20664	4.49	2.0E-04	M86524.1	NT	Human dystrophin gene
1162	11075		4	2.0E-04	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1856062 3' similar to contains MER3.b2 MER3 repetitive element ;
1169	11081		1.99	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1791	11689		1.44	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
2136	12024		1.29	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;
2528	12402	22293	4.15	2.0E-04	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
2958	12865	22683	1	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3389	13307	23105	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3417	13334	23138	0.98	2.0E-04	U34374.1	NT	Human tyrosine kinase TXK (txk) gene, exons 9 and 10
3837	13748	23541	0.78	2.0E-04	AW978441.1	EST_HUMAN	EST390550 MAGE resequences, MAGP Homo sapiens cDNA
4051	13953		4.61	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4569	14461	24249	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4569	14461	24250	1.27	2.0E-04	H96265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4689	14575		1.31	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
4991	14866	24630	1.7	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5403	15322	25371	1.63	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5411	15331	25381	1.68	2.0E-04	AI690862.1	EST_HUMAN	tq03b11.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207709 3'
6291	16155		2.5	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
6493	16352		11.07	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6497	16356	26527	1.6	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
6638	16518	26708	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6638	16518	26709	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6819	16698	26890	1.19	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6819	16698	26891	1.19	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6982	16859	27054	2.29	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7729	17579	27801	1.46	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
7754	17604	27828	1.71	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742964 5'
8225	18107	28360	6.14	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
8515	18387		1.88	2.0E-04	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8625	18490	28762	5.57	2.0E-04	AI440282.1	EST_HUMAN	tj01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
8726	18582	28866	2.94	2.0E-04	AW136740.1	EST_HUMAN	UI-H-BI1-adm-c-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
750	10680	20516	0.98	1.0E-04	H99646.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element ;
1059	10976	20819	2.43	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1098	11014	20855	3.87	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1098	11014	20856	3.87	1.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1310	11216		2.97	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1610	11515	21374	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamidine synthase, and LAMP (LAMP) genes, complete cds
1610	11515	21375	3.24	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen; ORF K14, v-GPCR, putative phosphoribosylformylglycinamidine synthase, and LAMP (LAMP) genes, complete cds
1817	11714	21594	1.67	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2600	12469	22363	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2600	12469	22364	1.29	1.0E-04	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
2655	12522	22411	1.15	1.0E-04	BE218833.1	EST_HUMAN	hv45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2655	12522	22412	1.15	1.0E-04	BE218833.1	EST_HUMAN	hv45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3247	13170	22969	1.04	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3675	13589	23376	1.1	1.0E-04	AI440282.1	EST_HUMAN	tj01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
3971	13878	23654	1.78	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
3991	13898	23675	1.08	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBBD04 3'
4362	14258	24043	0.85	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5028	14901	24671	1.56	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5028	14901	24672	1.56	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5033	14905	24676	0.99	1.0E-04	AI357156.1	EST_HUMAN	qx62h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
5148	15015		0.9	1.0E-04	Z72560.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL038c
5572	15487	25563	1.36	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6264	16129	26283	12.77	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
6468	16129	26283	14.47	1.0E-04	AI251980.1	EST_HUMAN	qv57d10.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
7380	17249	27455	2.53	1.0E-04	AI806220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
7384	17253	27458	1.46	1.0E-04	O88969	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
7562	17413	27628	1.75	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
7848	17698		3	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8649	18513		2.17	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8913	18721	29012	1.98	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
9035	18824		1.84	1.0E-04	BE696769.1	EST_HUMAN	CM0-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA
9566	19158		1.65	1.0E-04	AW893325.1	EST_HUMAN	CM2-NN0010-220300-124-d08 NN0010 Homo sapiens cDNA
683	10616	20439	1.7	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
3995	13902	23678	0.8	9.0E-05	AI762209.1	EST_HUMAN	wi54c11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.t1 MER6 repetitive element ;
5628	15543	25632	1.47	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7456	17264		2.9	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
7457	17266	27470	2.93	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
8479	18352	28617	2.6	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.t2 L1 repetitive element ;
8568	18436	28705	1.85	9.0E-05	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
8890	15543	25632	4.4	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
9329	19608		4.17	9.0E-05	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
804	10733	20576	1.46	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
846	10773		3.53	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2920	12847		0.78	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4852	15080		1.16	8.0E-05	F28172.1	EST_HUMAN	HSPD16734 HM3 Homo sapiens cDNA clone s3000003H04
8491	18364	28630	1.87	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9911	19589		3.45	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element;contains element MSR1 repetitive element ;
344	10303	20118	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
344	10303	20119	2.9	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
555	10496	20302	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
555	10496	20303	1.05	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1039	10957	20800	2.32	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2686	12551	22440	5.24	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3121	13046	22843	5.78	7.0E-05	AB009080.1	NT	Dictyostelium discoideum gene for TRFA, complete cds
4276	14175	23953	1.27	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4344	14241	24023	0.82	7.0E-05	U60980.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
4842	14723	24506	0.84	7.0E-05	9845300	NT	Rat cytomegalovirus Maastricht, complete genome
5202	16065		1.12	7.0E-05	AA367612.1	EST_HUMAN	EST78713 Placenta I Homo sapiens cDNA
7508	17296	27505	3.04	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBED60
8501	18374		2.89	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
1981	11874	21766	1.67	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1981	11874	21767	1.57	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2544	12418	22309	1.42	6.0E-05	AI655241.1	EST_HUMAN	wb54h06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN);
2652	12519	22409	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2652	12519	22410	0.89	6.0E-05	Z84506.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2783	10598	20415	2.45	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5605	15519	25599	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5605	15519	25600	3.33	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5855	15761	25879	1.49	6.0E-05	N72829.1	EST_HUMAN	yv50g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
6918	16796	26989	2.61	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
7330	17234	27437	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7330	17234	27438	1.37	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
7484	17354	27558	1.28	6.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
8131	18019	28267	3.68	6.0E-05	R75639.1	EST_HUMAN	yi59d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element;contains LTR7 repetitive element ;
8807	18621	28911	3.59	6.0E-05	AA044015.1	EST_HUMAN	zk58f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
9534	19587	25073	8.44	6.0E-05	AW890110.1	EST_HUMAN	MR0-NT0038-250400-001-f09 NT0038 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9965	19427		1.54	6.0E-05	BE858403.1	EST_HUMAN	7g28a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3307766 3'
1382	11287	21141	14.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1819	11716		1.63	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2831	12760	22550	0.88	5.0E-05	AJ251058.1	NT	Homo sapiens MEP1A gene, promoter region and exon 1
3897	13807	23593	2.99	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5392	15311	25165	9.01	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
5646	15559	25652	3.46	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCDMA06 3'
9326	19173		2.96	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
9590	19173		3.47	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2776	10193		4.58	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
7486	17356		7.17	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
8150	18038	28286	4.6	4.0E-05	AW627946.1	EST_HUMAN	hl36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element ;
9287	18989		2.17	4.0E-05	AW117580.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
665	10599	20417	0.84	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element ;
1043	10961	20804	1.36	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1115	11030	20870	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
1115	11030	20871	1.28	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3865142 5'
2688	12553	22442	0.91	3.0E-05	Q62234	SWISSPROT	SKELEMIN
4285	14184	23964	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4285	14184	23965	6.89	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4365	14261	24045	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4365	14261	24046	1.19	3.0E-05	AA368679.1	EST_HUMAN	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein
4519	14412	24197	0.85	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4731	10599	20417	0.84	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element ;
5151	15018	24786	0.97	3.0E-05	AV726630.1	EST_HUMAN	AV726630 HTC Homo sapiens cDNA clone HTCCEA01 5'
5412	15332	25382	1.54	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6611	16491	26677	2.23	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
6863	16742	26935	1.62	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
7154	17031	27225	1.65	3.0E-05	AW770982.1	EST_HUMAN	hl94e08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
7158	17035	27228	1.5	3.0E-05	6912431	NT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
7373	17242	27447	1.33	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7570	17421		3.15	3.0E-05	AI769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
2276	12160	22058	1.76	2.0E-05	AI286021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
2538	12412	22302	3.02	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2681	12546		7.21	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element;contains element L1 repetitive element ;
3098	13025	22821	1.5	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3304	13225	23027	0.94	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3323	13243	23050	1.14	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3449	13366		1	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3737	13649		0.85	2.0E-05	AL039107.1	EST_HUMAN	DKFZp566I064_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566I064 5'
4510	14403	24191	0.99	2.0E-05	AI263349.1	EST_HUMAN	qq13a08.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932374 3' similar to contains MER18.b3 MER18 repetitive element ;
4592	14480		1.06	2.0E-05	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
4782	14666	24453	0.81	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5520	15438	25502	1.42	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5993	15898	26022	2.19	2.0E-05	AA714330.1	EST_HUMAN	nw06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6125	15972	26108	2.19	2.0E-05	Y08926.1	NT	P.falciparum mRNA for AARP1 protein, partial
6136	15983		8.04	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6243	16109	26260	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6243	16109	26261	2.21	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6603	16483	26671	2.3	2.0E-05	AI381040.1	EST_HUMAN	tg20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
8024	17874	28116	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
8024	17874	28117	2.45	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
8039	15983		2.42	2.0E-05	AI991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
8748	17897	28141	2.93	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
9335	19514		2.98	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2 ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9442	19677		3.73	2.0E-05	AW074604.1	EST_HUMAN	xa89a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element ;
9486	19503		2.25	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) *gene, complete cds*
9637	19208	25257	1.81	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2663	12729	22417	1.61	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3599	13513	23301	1.67	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3886	13797	23583	9.24	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4082	13984	23761	1.09	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4180	14080	23853	2.01	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4742	14627	24413	2.16	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
4882	14763	24539	4.46	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6049	15952	26082	1.42	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
6211	15993	26128	3.54	1.0E-05	AA641846.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element ;
6213	16079	26228	6.45	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6572	16430		1.8	1.0E-05	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7168	17045		2.18	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7240	17117	27312	2.48	1.0E-05	AA452578.1	EST_HUMAN	zx35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
7352	17220	27420	11.8	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element;contains element TAR1 repetitive element ;
7704	17554	27778	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7704	17554	27779	1.2	1.0E-05	AW291521.1	EST_HUMAN	UI-H-BI2-agk-a-08-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
7851	17701		1.78	1.0E-05	AW466995.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.t2 L1 repetitive element ;
8291	18170	28414	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8291	18170	28415	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2637	12504	22398	6.59	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3057	12984	22775	3.66	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3559	13473		2.94	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5599	15513	25591	2.58	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6570	16428	26611	10.24	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element;
6931	16809	27004	1.16	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7192	17069	27257	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7192	17069	27258	2.81	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7317	17193	27394	4.58	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
8309	18186	28434	3.35	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2483	12722	22251	1.55	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
8992	18796	29087	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
8992	18796	29088	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
963	10886		1.7	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ;
1420	11326	21191	3.19	7.0E-06	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2844	12772		6.66	7.0E-06	AI368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3516	13432		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5493	15412		5.73	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
9072	19698	24900	5.39	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2887	12814	22607	1.09	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3635	13549	23336	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4647	12838	22637	1.77	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4663	14539	24328	2.01	6.0E-06	AI040099.1	EST_HUMAN	ox08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.t2 MER8 repetitive element ;
5281	15203	24979	1.46	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
7670	17520		1.88	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
9900	19377	26195	1.8	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5695	15604	25706	3.58	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5825	15731	25843	1.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7817	17667	27907	6.9	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9795	19311	25204	4.74	5.0E-06	AI065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
631	10568	20380	4.41	4.0E-06	R16267.1	EST_HUMAN	ya48c03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element;contains L1 repetitive element ;
828	10755	20605	9.3	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element;contains element MER21 repetitive element ;
1312	11218	21074	5.18	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1312	11218	21075	5.18	4.0E-06	AI334928.1	EST_HUMAN	tb33e09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1458	11363	21227	2.23	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2218	12104	22008	1.22	4.0E-06	AW015401.1	EST_HUMAN	UI-H-BI0-aat-f-05-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3025	12953	22746	1.39	4.0E-06	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3819	13731	23520	1.78	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4702	14588	24378	1.58	4.0E-06	AI886939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element ;
4840	14721	24504	1.02	4.0E-06	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7109	16986	27177	3.1	4.0E-06	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8746	17895	28139	3.74	4.0E-06	AB007955.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2117	12006	21904	1.27	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element ;
2117	12006	21905	1.27	3.0E-06	AA700562.1	EST_HUMAN	zi34b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.t1 L1 repetitive element ;
2220	12105		1.37	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2891	12818	22610	0.95	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.t3 LTR1 repetitive element ;
3228	13152		2.14	3.0E-06	AI857779.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN ;contains L1.t2 L1 repetitive element ;
3716	13628	23412	1.26	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3716	13628	23413	1.26	3.0E-06	BE047094.1	EST_HUMAN	hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4376	14272	24053	0.9	3.0E-06	T50266.1	EST_HUMAN	yb78b10.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4461	14355	24146	4.31	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
6290	16154		1.92	3.0E-06	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9494	19110		4.17	3.0E-06	AW385262.1	EST_HUMAN	RC0-LT0001-281199-011-A03 LT0001 Homo sapiens cDNA
195	10167		3.28	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1550	11455		6.27	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2326	12207	22106	2.95	2.0E-06	AI672138.1	EST_HUMAN	wa04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element ;
2418	12295	22192	2.14	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2519	12393	22285	2.69	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3475	13391	23196	1.11	2.0E-06	AV657555.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3700	13614	23398	1.5	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3710	13623	23406	1.5	2.0E-06	AB030896.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5878	15784	25904	5.08	2.0E-06	AI819424.1	EST_HUMAN	wj90b04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7136	17013	27206	1.65	2.0E-06	H62051.1	EST_HUMAN	yu37c04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929 KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
9403	19699	24901	1.35	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
9548	19148		2.46	2.0E-06	BE328232.1	EST_HUMAN	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.t2 L1 repetitive element ;
31	10018	19813	1.9	1.0E-06	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
641	10578	20394	1.61	1.0E-06	AF084364.1	NT	Mus musculus D6MM5E protein (D6Mm5e) mRNA, complete cds
1435	11340	21206	2.22	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1507	11412	21271	1.09	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1554	11459	21317	0.93	1.0E-06	AA034141.1	EST_HUMAN	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1554	11459	21318	0.93	1.0E-06	AA034141.1	EST_HUMAN	zi06a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429982 3' similar to contains Alu repetitive element;
1565	11470		1.2	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1949	11844	21729	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1949	11844	21730	4.74	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	14172	23949	11.11	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5043	14915	24688	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5043	14915	24689	1.38	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5233	15157	24925	4.69	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
6107	16001	26139	6.11	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
6813	16692	26881	1.16	1.0E-06	AI347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926842 3'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6944	16822	27013	1.53	1.0E-06	AI287878.1	EST_HUMAN	qv23f06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
7582	17433	27647	3.72	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7582	17433	27648	3.72	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
7609	17460	27676	4.86	1.0E-06	AA132611.1	EST_HUMAN	zo17e08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
7637	17488		3.73	1.0E-06	AA449257.1	EST_HUMAN	zx04d11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
7989	17839		1.52	1.0E-06	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8912	18720		4.81	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
9440	19077	25280	2.99	1.0E-06	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
9536	11844	21729	1.84	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
9536	11844	21730	1.84	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
357	10314	20134	1.49	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
367	10314	20135	1.49	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8572	18440	28708	2.38	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4661	14547	24336	4.49	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4661	14547	24337	4.49	8.0E-07	AI288596.1	EST_HUMAN	ql82g07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
5589	15504		7.45	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6667	16547		7.89	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8893	18703		7.2	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBEN89
9055	18838		4.15	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1822	11719	21599	0.94	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
1870	11766	21641	2.36	6.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
2442	12319	22217	2.41	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3891	13802		1.65	6.0E-07	P41479	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
7279	17156	27351	1.35	6.0E-07	BF001867.1	EST_HUMAN	7g94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L. ;
9303	19653		1.81	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
323	10284		3.55	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1041	10959		2.9	5.0E-07	AA380630.1	EST_HUMAN	EST93615 Supt cells Homo sapiens cDNA 5' end
2995	12923		0.87	5.0E-07	AI831893.1	EST_HUMAN	wh64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4547	14440	24223	1.44	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6203	15963	26096	1.71	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element;contains element A3R repetitive element ;
6203	15963	26097	1.71	5.0E-07	AI393981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element;contains element A3R repetitive element ;
6348	16211	26373	15.93	5.0E-07	AW070885.1	EST_HUMAN	xa31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
7932	17782	28021	4.11	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
8805	18619	28909	4.31	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8863	18675		2.06	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
9712	19556		2.02	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
3918	13827	23608	1.98	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
7235	17112	27305	5.29	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
8308	18185	28432	3.84	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
8308	18185	28433	3.84	4.0E-07	AI765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703 3'
8552	18422		2.05	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
434	10379	20200	6.01	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
568	10507	20314	2.38	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1352	11258	21114	2.19	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1608	11513		2.23	3.0E-07	M64857.1	NT	Human IgK subgroup I germline gene, exons 1 and 2, V-region 018 allele
2000	11893		1.01	3.0E-07	AA526763.1	EST_HUMAN	nl56b09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element;contains L1.t3 L1 repetitive element ;
2242	12126	22026	1.15	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2420	12297	22194	17.25	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2420	12297	22195	17.25	3.0E-07	BE005077.1	EST_HUMAN	MR0-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2998	12926	22718	0.85	3.0E-07	T84704.1	EST_HUMAN	yd50f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111695 5'
3122	13047	22844	1.82	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4624	14512	24302	7.05	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCCD01 3'
4654	14540	24329	0.89	3.0E-07	AI797236.1	EST_HUMAN	we86b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
4996	14871	24634	1.47	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
4996	14871	24635	1.47	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5476	15396	25462	10.26	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6026	15930		5.32	3.0E-07	AA815175.1	EST_HUMAN	oc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
6433	16294	26456	3	3.0E-07	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
8918	18726		3	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9939	19408		2.76	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
26	10013	19807	2.62	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
148	10122	19940	4.75	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
148	10122	19941	4.75	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
175	10146	19962	116.1	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
731	10663	20495	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	10663	20496	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	10853	20701	3.11	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN);contains Alu repetitive element;
929	10854	20702	3.38	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1147	11060	20903	1.28	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1582	11486	21347	1.84	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I
3633	13547	23334	14.74	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5078	14948	24723	0.97	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS ;
5078	14948	24724	0.97	2.0E-07	AW070995.1	EST_HUMAN	xa05h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C38H2.1 CE00923 PROBABLE RABGAP DOMAINS ;
5198	15061	24826	0.95	2.0E-07	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5277	15199	24975	1.73	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6009	15914	26041	1.69	2.0E-07	AI208715.1	EST_HUMAN	qg56d05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
6934	16812		3.91	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
7627	17478		1.61	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7891	17741	27984	6.48	2.0E-07	AW892507.1	EST_HUMAN	CM4-NN0003-280300-124-e06 NN0003 Homo sapiens cDNA
9094	19557		1.48	2.0E-07	AI732462.1	EST_HUMAN	zn85h11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element ;
1086	11002		1.21	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12280	22177	0.94	1.0E-07	7549818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2797	11410	21269	1.75	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3684	11002		1.33	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4195	14095	23874	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4195	14095	23875	2.37	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6103	15997	26132	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
6103	15997	26133	5.2	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
6424	16285	26447	9.04	1.0E-07	N65081.1	EST_HUMAN	yv43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
6782	16661	26850	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
6782	16661	26851	2.81	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7180	17057	27246	3.24	1.0E-07	AA693576.1	EST_HUMAN	zi51e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homp sapiens cDNA clone IMAGE:434346 3'
7714	17564	27790	2.37	1.0E-07	BF674524.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
7716	17566	27792	1.28	1.0E-07	AA386311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
7980	17830		1.56	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
9364	19533	25060	3.66	1.0E-07	BE048770.1	EST_HUMAN	hr53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O95722 O95722 DJ1163J1.1 ;
9497	19113		1.37	1.0E-07	X64467.1	NT	H.sapiens ALAD gene for porphobilinogen synthase
9661	19222		4.61	1.0E-07	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
7689	17539	27765	1.67	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'
8520	18392	28656	2.91	9.0E-08	AI891052.1	EST_HUMAN	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.t2 OFR repetitive element ;
8922	18730	29025	3.91	9.0E-08	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9316	19008		3.09	9.0E-08	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
591	12671		2.65	8.0E-08	AI911352.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
1034	10952		0.88	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3498	13415		1.43	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
7074	16951	27144	3.38	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7074	16951	27145	3.38	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7551	17402	27616	2.89	8.0E-08	AW970693.1	EST_HUMAN	EST382776 MAGE resequences, MAGK Homo sapiens cDNA
8570	18438		2.39	8.0E-08	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
73	10057	19874	3.27	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1338	11244	21102	12.71	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3528	13444	23240	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	13444	23241	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8189	18075		4.63	7.0E-08	AI535743.1	EST_HUMAN	cong3.P11.A5 conorm Homo sapiens cDNA 3'
8926	18734	29027	5.6	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
9770	13444	23240	4.54	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9770	13444	23241	4.54	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9834	19334		1.89	7.0E-08	AJ131016.1	NT	Homo sapiens SCL gene locus
800	10729	20569	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10729	20570	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12193	22092	1.73	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0166-191199-004-g09 HT0166 Homo sapiens cDNA
4155	14055	23829	0.99	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8717	18534	28818	2.26	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8819	18632		1.74	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
79	10063	19880	3.06	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	12076	21981	1.97	5.0E-08	AA493851.1	EST_HUMAN	nh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
6178	16042	24809	1.12	5.0E-08	Q06278	SWISSPROT	ALDEHYDE OXIDASE
9057	18839		4.36	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
9245	18958	25317	1.94	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1724	11625	21493	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21494	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
7278	17155	27350	1.41	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
7938	17788	28030	4.17	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
8274	18154		1.79	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
8439	18313	28570	3.66	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
8439	18313	28571	3.66	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
9061	19680		1.54	4.0E-08	W76159.1	EST_HUMAN	zd65g03.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.t1 L1 repetitive element ;
9703	19252		1.46	4.0E-08	AI343353.1	EST_HUMAN	tb95a11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5184	15048	24812	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5184	15048	24813	7.24	3.0E-08	AA191195.1	EST_HUMAN	zq45d05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632649 5'
5446	15367	25423	1.99	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
6163	15120	24864	3.58	3.0E-08	AI792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5'
6451	16312	26478	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6558	16416		2.97	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9027	18819		11.6	3.0E-08	R18420.1	EST_HUMAN	yg02f04.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
199	10171		15.76	2.0E-08	AW302996.1	EST_HUMAN	xr87f06.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
223	10194		7.97	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element;contains element MER15 repetitive element ;
488	10431	20245	1.48	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
644	10581	20396	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
644	10581	20397	10.93	2.0E-08	AW886438.1	EST_HUMAN	MR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
974	10898		37.42	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1319	11226	21082	1.93	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1707	11608		1.03	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1811	11708		3.99	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2368	12248	22140	1.42	2.0E-08	AA731948.1	EST_HUMAN	nw64h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.t3 L1 repetitive element ;
2496	12371		2.16	2.0E-08	K00216.1	NT	Sheep His-tRNA-GUG
3171	13096	22901	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3171	13096	22902	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3783	13695		1.66	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
3986	13893	23669	0.78	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4305	14203		3.35	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.t2 L1 repetitive element ;
4876	14756		2.89	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element;
6722	16602	26791	1.31	2.0E-08	AA490121.1	EST_HUMAN	ab02g06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
8995	18799	29092	11.62	2.0E-08	BF589904.1	EST_HUMAN	naa32e09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3257969 3'

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1493	12696	21257	1.13	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2005	11897		2.92	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-160999-001-f12 HT0130 Homo sapiens cDNA
3155	13080	22881	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3155	13080	22882	1.24	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5191	15054	24818	1.43	1.0E-08	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5438	15358	25414	4.05	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-60
6975	16852	27045	1.84	1.0E-08	AI015304.1	EST_HUMAN	ot35a05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
8633	18498	28773	3.66	1.0E-08	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
9434	19074		2.01	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9804	19316		6.3	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9894	19518		1.76	1.0E-08	BF375398.1	EST_HUMAN	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4149	14049	23823	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4149	14049	23824	2.98	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3444	13361		1.07	8.0E-09	BE012076.1	EST_HUMAN	RC5-BN1058-270400-031-C06 BN1058 Homo sapiens cDNA
6307	16171	26328	6.12	8.0E-09	AI183500.1	EST_HUMAN	qd42e07.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.t1 MSR1 repetitive element ;
6666	16546	26743	2.71	8.0E-09	AW900159.1	EST_HUMAN	CM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
7196	17073		3.06	8.0E-09	AA938892.1	EST_HUMAN	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3555	13469		1.68	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4558	14450	24236	0.99	7.0E-09	D00649.1	NT	Homo sapiens gene for enteric smooth muscle gamma-actin, exon 2, 3
7335	17203	27403	3.27	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
7850	17700	27945	1.84	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
2107	11996		1.06	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
3941	13849	23625	1.06	6.0E-09	AA557940.1	EST_HUMAN	nl17a11.s1 NCI_CGAP_HSC1 Homo sapiens cDNA clone IMAGE:1040924 similar to contains L1.t2 L1 repetitive element ;
4906	14786	24562	4.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5305	15226	25030	8.19	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
7294	17170	27370	2.26	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7896	17746		4.06	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
1394	11299	21157	3.09	5.0E-09	BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5858	15764	25881	1.92	5.0E-09	AA359454.1	EST_HUMAN	EST68746 Fetal lung II Homo sapiens cDNA 5' end
7811	17661	27901	2.69	5.0E-09	AW799667.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
510	10452		1.68	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
949	10873		2.31	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1453	11358	21222	0.95	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2379	12259	22151	6.36	4.0E-09	AA350878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2303	12184	22082	3.82	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;
2506	12380	22270	1.25	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;
2614	12482	22371	1.1	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3287	13208	23008	1.1	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.t3 MER18 repetitive element ;
4329	14226	24008	3.22	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4AI (EIF4A1) gene, partial cds
4411	14305	24088	1.54	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
7884	17734	27978	1.73	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8384	18261	28510	3.8	3.0E-09	BF109943.1	EST_HUMAN	7l72c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
8384	18261	28511	3.8	3.0E-09	BF109943.1	EST_HUMAN	7l72c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
795	10724		0.93	2.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
1237	11144	20995	5.23	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1637	11541		10.52	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2278	12162	22059	2.25	2.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3858	13769	23561	3.65	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6405	16266	26428	8.9	2.0E-09	AA461430.1	EST_HUMAN	zx63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7055	16932	27122	1.37	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
8589	18457	28726	2.11	2.0E-09	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9576	10724		11.53	2.0E-09	X16674.1	NT	H.sapiens PADPRP-I gene for NAD(+) ADP-ribosyltransferase
9640	19749		1.62	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1093	11009	20850	2.48	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1093	11009	20851	2.48	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616	11520		0.95	1.0E-09	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2453	12330		0.94	1.0E-09	AI356086.1	EST_HUMAN	qy64e11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.t2 MER12 repetitive element ;
2860	12788	22580	1.51	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2895	12822	22614	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2895	12822	22615	3.25	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2949	12876	22674	1.23	1.0E-09	P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]
3002	12930	22722	0.78	1.0E-09	BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4692	14578		4.26	1.0E-09	AA719297.1	EST_HUMAN	zh35b03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
5560	15476	25549	1.37	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
5736	15644	25749	3.21	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7911	17761		3.1	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9478	19689	24996	2.14	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1287	11195	21048	1.8	9.0E-10	AW867740.1	EST_HUMAN	MR0-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2803	12733	22532	6.03	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element PTR5 repetitive element ;
6087	16032	26172	4.63	9.0E-10	AI452982.1	EST_HUMAN	tj46b09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:O00372 O00372 PUTATIVE P150. ;
141	10115	19935	9.43	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	23022	0.87	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-f01 BT0631 Homo sapiens cDNA
4106	14006	23782	2.82	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
7725	17575		2.32	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
9005	18808	29100	2.31	8.0E-10	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
686	10619	20444	12.45	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
686	10619	20445	12.45	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1605	11510	21371	1.87	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1974	11867		1.01	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	12386		16.88	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	12976	22768	2.65	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
5754	15662	25769	3.98	7.0E-10	AA345220.1	EST_HUMAN	EST51247 Gall bladder II Homo sapiens cDNA 5' end
6514	16373		1.39	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
895	10821	20666	2.81	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	6.0E-10	AI424405.1	EST_HUMAN	tf02d07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2095021 3'
4634	14622		2.51	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
9092	18865		1.79	6.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE resequences, MAGL Homo sapiens cDNA
9947	19597		3.54	6.0E-10	BE699410.1	EST_HUMAN	RC3-NN0070-110800-014-h07 NN0070 Homo sapiens cDNA
744	10675		4.5	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N219 5'
3430	13347	23152	1.48	5.0E-10	Q01033	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
6334	16197		1.82	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7496	17366	27570	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
7496	17366	27571	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
106	10087		0.99	4.0E-10	AI221083.1	EST_HUMAN	qg09f09.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element ;
1951	11846	21732	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;
2527	12401	22292	6.09	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6259	16125	26278	19.23	4.0E-10	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8436	18310		7.7	4.0E-10	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
897	10822	20668	1.72	3.0E-10	N36113.1	EST_HUMAN	yy32f06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.t1 L1 repetitive element ;
1329	11236		6.63	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
4435	14330	24117	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4435	14330	24118	1.1	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5765	15672	25779	2.83	3.0E-10	P20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
5833	15739	25851	3.27	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906319 5'
6562	16420	26599	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
6562	16420	26600	1.31	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7067	16944	27136	1.58	3.0E-10	H87208.1	EST_HUMAN	ys74b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element ;
7233	17110	27302	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7233	17110	27303	1.47	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
7979	17829		2.56	3.0E-10	T65891.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8026	17876		1.54	3.0E-10	AA769294.1	EST_HUMAN	nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
9737	19271	25227	2.03	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
32	10019	19814	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
32	10019	19815	1.43	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1855	11751		5.91	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
5547	15463		2.41	2.0E-10	Q28640	SWISSPROT	(HPRG)
5787	15693	25801	1.71	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6367	16230	26389	5.79	2.0E-10	BE791082.1	EST_HUMAN	601586208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
1492	11397		3.56	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-290300-001-f01 SN0038 Homo sapiens cDNA
1589	11493	21353	3.14	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2537	12411		2.4	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191199-058-e08 CT0225 Homo sapiens cDNA
3456	13372	23178	0.89	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161199-013-g10 TT0003 Homo sapiens cDNA
3770	13411		0.91	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3933	13842		5.44	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4036	13939	23716	4.61	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4036	13939	23717	4.51	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4042	13945	23724	2.25	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXXC domain 1, complete cds
4079	13981		2.06	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
5145	15012		0.93	1.0E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
7859	17709		4.59	1.0E-10	AA081868.1	EST_HUMAN	zn23g06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548314 5'
8286	18165	28408	3.4	1.0E-10	AI038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
9037	15012		1.43	1.0E-10	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
9084	18859		1.3	1.0E-10	AA397885.1	EST_HUMAN	zt88b10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729211 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
261	10226	20042	1.2	9.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2057	11947	21843	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
2057	11947	21844	5.43	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23064	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
3337	13257	23065	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4400	14295	24079	1.09	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5421	15342		4	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
9410	19062	25312	2.69	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3078	13005		9.97	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element ;
3881	13792	23580	0.83	8.0E-11	AI478617.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3957	13865	23641	4.03	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
1431	11336	21202	2.11	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
6949	16827	27020	2.55	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7873	17723		1.22	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9545	19145		1.31	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'
406	10352	20180	5.16	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
406	10352	20181	5.16	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6529	16388	26568	3.58	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6871	16750	26945	6.49	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
11	9997	19788	0.92	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3320	9997	19788	1.48	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4135	14035	23811	1.49	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5926	15831	25954	1.69	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
6446	16307	26472	14.59	5.0E-11	11416799	NT	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA
8975	18780	29072	1.79	5.0E-11	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1380	11285		1.4	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2760	12622	22514	8.45	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909295 5'
4518	14411	24196	1.37	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
5897	15803	25927	2.94	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6362	16225		3.66	4.0E-11	AF224669.1	NT	Homo sapiens mannosidase; beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7405	17272		1.59	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-f08 HT0256 Homo sapiens cDNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9611	19190	25252	1.93	4.0E-11	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1476	11381	21245	2.15	3.0E-11	6679077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
4179	14079		1.45	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
944	10869	20716	1.58	2.0E-11	AI150502.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.t3 MER10 repetitive element ;
1168	11080	20926	3.64	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1168	11080	20927	3.64	2.0E-11	R24807.1	EST_HUMAN	yg43e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35144 5'
1596	11500	21359	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1596	11500	21360	3.91	2.0E-11	L17432.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3'beta (COR3'beta) genes, complete cds
1600	11505	21365	1.04	2.0E-11	AI126371.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);contains L1.t1 L1 repetitive element ;
2737	12599	22493	1.11	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3160	13085	22889	4.23	2.0E-11	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3284	13205	23005	0.87	2.0E-11	AI478617.1	EST_HUMAN	tm54c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
3452	13368		0.95	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4501	14395		0.97	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4851	14732		5.46	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA
4961	14836	24604	1.32	2.0E-11	AA307331.1	EST_HUMAN	EST178226 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2-macroglobulin
5810	15715	25828	1.83	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW:PR16_YEAST P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16. ;
7318	17194		1.43	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7900	17750	27989	4.61	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 5I1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
8457	18330	28591	2.07	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
8457	18330	28592	2.07	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
9160	19679		1.29	2.0E-11	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
9192	18927		2.25	2.0E-11	AW842143.1	EST_HUMAN	RC0-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
9216	18943	25356	1.98	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
9477	19103		1.89	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9627	19201		2.38	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9930	19401		2.38	2.0E-11	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
660	10594	20412	1.24	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
1199	11109	20954	2.58	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1483	11388		1.94	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2079	11969	21862	3.12	1.0E-11	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
3454	13370	23174	1.32	1.0E-11	BE004316.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5269	15191	24966	14.34	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6773	16652	26840	3.25	1.0E-11	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
6989	16866	27060	5.41	1.0E-11	R13174.1	EST_HUMAN	yf73d08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28166 5'
7232	17109	27300	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
7232	17109	27301	1.32	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
8607	18474	28747	1.9	1.0E-11	BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295977 5'
9702	19483		1.29	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
2922	12849	22649	0.82	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
7641	17491	27712	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7641	17491	27713	1.22	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9270	18974		3.57	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
4562	14454	24241	2.75	7.0E-12	Q05904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
8656	18545	28828	11.23	7.0E-12	AA704735.1	EST_HUMAN	zj23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461152 3'
3500	13417		0.92	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4252	14151	23925	7.85	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
7201	17078	27263	1.19	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
7453	17262		1.86	6.0E-12	AA847898.1	EST_HUMAN	od10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29.t2 MER29 repetitive element ;
1027	10945	20790	2.88	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDV33
3344	13264	23070	1.18	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
3666	13580	23367	5.93	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
5171	15037		0.84	5.0E-12	AA720661.1	EST_HUMAN	nw24b11.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241373 3'
5667	15578	25676	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5667	15578	25677	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5909	15815	25940	9.12	5.0E-12	AW974760.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
7268	17145	27339	2.15	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7895	17745		4.67	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
244	10211	20027	3.42	4.0E-12	AA700326.1	EST_HUMAN	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	10211	20027	3.55	4.0E-12	AA700326.1	EST_HUMAN	zj74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4520	14413	24198	0.85	4.0E-12	AI689984.1	EST_HUMAN	tx26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
6797	16676		2.89	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8431	18305	28561	3.51	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9520	19131		1.9	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
600	10536	20345	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
600	10536	20346	3.81	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP. ;
8047	17938	28187	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
8047	17938	28188	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3421	13338	23143	1.03	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4025	13928	23704	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4025	13928	23705	1.04	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4324	14221		1.8	2.0E-12	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	14688	24473	0.78	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5898	15804		2.22	2.0E-12	AW971857.1	EST_HUMAN	EST383946 MAGE resequences, MAGL Homo sapiens cDNA
6258	16124	26277	3.34	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
6516	16376	26552	2.07	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7367	17345		1.68	2.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7737	17587		8.13	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9175	18916		1.71	2.0E-12	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9377	19041		1.52	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
117	10095	19914	1.82	1.0E-12	AW627674.1	EST_HUMAN	hh90a09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1 MER18 repetitive element ;
1944	11839		2.03	1.0E-12	AI871726.1	EST_HUMAN	wm51f07.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1 repetitive element ;
3032	12960	22762	1.16	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3032	12960	22753	1.16	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3798	13710	23496	27.7	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3798	13710	23497	27.7	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
5630	15544		1.73	1.0E-12	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
5682	15591		1.82	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6224	16090	26240	1.72	1.0E-12	AF196864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
6240	16106	26256	9.11	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element ;
6240	16106	26257	9.11	1.0E-12	AI248533.1	EST_HUMAN	qh66a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849614 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.t1 MER10 repetitive element ;
7051	16928	27119	1.31	1.0E-12	AA782323.1	EST_HUMAN	ac26d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
9085	18860	29118	3.36	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
9605	19728		2.2	1.0E-12	P44836	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR
9963	19426		2.72	1.0E-12	X85949.1	NT	M.setulosus mitochondrial 12S rRNA gene
3575	13489		1.13	9.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
3865	13776	23570	1.16	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
7537	17388		2.37	9.0E-13	N69653.1	EST_HUMAN	za26b06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
700	10633	20458	5.05	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
700	10633	20459	5.05	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1796	11694	21570	1.36	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
7838	17688		2.13	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8984	18789	29079	2.49	8.0E-13	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
9550	19149		10.33	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
9768	19287		1.33	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2054	11944	21840	18.51	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3280	13201		1.05	5.0E-13	R78338.1	EST_HUMAN	yl82f04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3351	13271		1.45	5.0E-13	AA435773.1	EST_HUMAN	zt77a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
8234	18115	28367	2.75	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1824	11721		2.96	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
2411	12288		1.58	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5430	15350	25404	4.86	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6278	16142	26298	1.92	4.0E-13	AB037750.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
6542	16400		1.52	4.0E-13	N44291.1	EST_HUMAN	yy33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995 A32995 t complex sterility protein - mouse ;
7757	17607	27831	4.67	4.0E-13	AI289831.1	EST_HUMAN	qn32d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu repetitive element;
8507	18379	28645	1.83	4.0E-13	AA435819.1	EST_HUMAN	zt78g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
8507	18379	28646	1.83	4.0E-13	AA435819.1	EST_HUMAN	zt78g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
173	10144		3.8	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
847	10774		1.37	3.0E-13	AA430310.1	EST_HUMAN	zw68g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2319	12200	22099	1.25	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
2429	12306		2.63	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2629	12497	22387	4.23	3.0E-13	BF372962.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3150	13075		2.86	3.0E-13	AA745844.1	EST_HUMAN	ob18d02.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324036 3'
6601	16481	26669	5.92	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8064	17955		4.03	3.0E-13	AI064768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
8403	18279	28531	3.66	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
8876	18688	28980	2.6	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
144	10118	19938	2.77	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
239	10207	20024	1.31	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1249	11156	21005	4.71	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3244	13167	22966	1.08	2.0E-13	BF431899.1	EST_HUMAN	nab76f05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4019	13923		1.72	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5722	15629	25732	3.87	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6078	16061	26209	6.32	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7976	17826	28067	3.97	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
9251	18961		7.42	2.0E-13	AW892155.1	EST_HUMAN	CM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
288	10252	20072	1.37	1.0E-13	S74129.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
870	10796	20646	4.39	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1314	11220	21077	1.27	1.0E-13	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1976	11869	21761	2.16	1.0E-13	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
4488	14382	24169	1.48	1.0E-13	BF340987.1	EST_HUMAN	602038009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185866 5'
8684	18572	28855	13.83	1.0E-13	BF108755.1	EST_HUMAN	7l45e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
9076	18853		1.62	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
9714	19255		1.6	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
330	10289	20105	2.92	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
331	10290	20106	2.85	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
2451	12328		4.04	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2725	12587	22482	4.62	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3073	13000	22790	3.74	9.0E-14	AW513296.1	EST_HUMAN	xo54h05.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707833 3'
3200	10289	20105	0.98	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element ;
3728	13640	23426	5.22	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4650	14536	24325	1.93	9.0E-14	AJ002153.1	NT	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin I
3463	13369		1.57	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3872	13783		2.77	8.0E-14	R76269.1	EST_HUMAN	yl72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
7434	16447	26637	60.69	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
7516	17303	27510	3.49	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
8732	18588		4.39	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-261099-014-a01 BT0258 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1611	12699		3.07	7.0E-14	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
363	10319	20140	10.2	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
5114	14982	24756	1.02	6.0E-14	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
5114	14982	24757	1.02	6.0E-14	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
7652	17502	27725	2.56	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7652	17502	27726	2.56	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
602	10538	20348	3.92	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4985	14860	24628	1.09	5.0E-14	AW073791.1	EST_HUMAN	xb03b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.t2 L1 repetitive element ;
5397	15316	25363	5.12	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1107	12685		1.77	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1835	11732	21608	6.5	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3693	13607		0.94	4.0E-14	AA046502.1	EST_HUMAN	zk67e06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4194	14094	23873	1	4.0E-14	N46328.1	EST_HUMAN	yy73c12.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.t3 L1 repetitive element ;
9777	19760		2.31	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
934	10859	20705	2.13	3.0E-14	X95466.1	NT	R.norvegicus mRNA for CPG2 protein
4841	14722	24505	0.82	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element ;
4844	14725	24507	1.1	3.0E-14	7656864	NT	Homo sapiens a disintegrin and metalloproteinase domain 29 (ADAM29), mRNA
6104	14972		1.23	3.0E-14	BE466372.1	EST_HUMAN	hx94f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3195601 3' similar to contains MER4.b2 MER4 repetitive element ;
5157	15024	24791	1.5	3.0E-14	P02894	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8563	14722	24505	7.59	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element ;
384	10331	20154	3.98	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
384	10331	20155	3.98	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
676	12673	20428	6.35	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2339	12219		1.36	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
2416	12293		1.09	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2479	12355	22246	1.24	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2640	12507		0.95	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5505	15423	25485	2.96	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6114	16008		2.18	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
6432	16293	26454	19.91	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
6432	16293	26455	19.91	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
8160	18048	28300	4.76	2.0E-14	AW139800.1	EST_HUMAN	UI-H-BI1-adw-a-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
8791	15423	25485	1.81	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
1051	10968	20810	1.31	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1384	11289	21143	7.67	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1384	11289	21144	7.67	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1956	11851	21738	21.54	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2137	12025	21921	6.17	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2358	12238	22134	6.43	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2914	12841	22641	1.38	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3130	13055	22854	4.67	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3130	13055	22855	4.67	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3811	13723	23512	2	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4374	14270	24051	1.74	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5550	15466	25536	1.97	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6012	19457	26045	10.41	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6012	19457	26046	10.41	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1558	11463	21320	2.85	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2126	12014		1.64	9.0E-15	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
6427	16288	26449	4.28	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
6673	16553	26748	1.53	9.0E-15	BE903559.1	EST_HUMAN	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
2780	10415		1	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7963	17813		2.83	7.0E-15	AW241958.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.t2 THR repetitive element ;
978	10901	20748	6.12	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
8622	19770		1.86	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
9948	19415		1.57	6.0E-15	BF432200.1	EST_HUMAN	nab81c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
404	10350	20177	5.79	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2733	12595	22490	1.38	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
3423	13340		1	6.0E-16	AW296817.1	EST_HUMAN	UI-H-BW0-ajb-g-10-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
8063	17954		2.22	5.0E-15	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
421	9988	19779	2.6	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4039	13942	23720	0.78	4.0E-15	AL118596.1	EST_HUMAN	DKFZp761C0810_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761C0810 5'
8414	16438	26623	2.38	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
8414	16438	26624	2.38	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4123	14023		5.93	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
4843	14724		1.41	3.0E-15	P92485	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4955	14832	24599	0.88	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
4955	14832	24600	0.88	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6314	16177	26335	2.86	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6314	16177	26336	2.86	3.0E-16	M27686.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7709	17559		1.87	3.0E-15	AA807128.1	EST_HUMAN	oc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.t1 MER19 repetitive element ;
8173	18061	28311	2.71	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	10216	20033	3.29	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced.
364	10320	20141	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
364	10320	20142	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1512	11417		1.14	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3465	13381	23186	1.04	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3465	13381	23187	1.04	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4522	14415		2.07	2.0E-15	AI806335.1	EST_HUMAN	wf07f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043 Q61043 NINEIN. ;
5097	14966	24741	1.33	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5097	14966	24742	1.33	2.0E-15	P13993	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6223	16089		1.71	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6310	16173	26331	2.2	2.0E-15	AA704195.1	EST_HUMAN	zj77e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
6375	16237	26397	5.13	2.0E-15	W05064.1	EST_HUMAN	za78d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:298675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
7163	17040	27232	2.72	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
7410	17277	27484	1.26	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
7410	17277	27485	1.26	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
8212	18096		3.01	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
9799	13381	23186	2.22	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9799	13381	23187	2.22	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2747	12609		1.84	1.0E-15	AI689984.1	EST_HUMAN	tx26h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
2979	12906	22706	0.8	1.0E-15	BE043584.1	EST_HUMAN	hk40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2999162 5'
3103	13029	22825	0.99	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4262	14161	23939	0.8	1.0E-15	BE182696.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT0649 Homo sapiens cDNA
5086	14956	24731	1.15	1.0E-15	AI984928.1	EST_HUMAN	wr86e04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494590 3'
5844	15750	25864	1.83	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
6182	16068		1.96	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
6791	16670	26862	1.28	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6905	16783	26976	4.57	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
6905	16783	26977	4.57	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
7227	17104	27293	1.44	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8193	18079	28331	6.81	1.0E-15	AF044083.1	NT	Homo sapiens major histocompatibility locus class III region
9867	19492	25131	3.71	1.0E-15	AI783944.1	EST_HUMAN	tr31c05.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
4404	14298	24082	1.03	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
8361	18238	28486	2.6	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
6343	16206	26368	1.5	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6343	16206	26369	1.5	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
9816	19585		6.8	7.0E-16	T94149.1	EST_HUMAN	ye28c12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
2094	11983		8.32	6.0E-16	AW972611.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1477	11382	21246	1.09	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2647	12514	22404	1.79	5.0E-16	AA992176.1	EST_HUMAN	ot80c04.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element ;
7784	17634	27867	1.69	5.0E-16	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8809	18623	28914	3.33	5.0E-16	BF217368.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
9904	19381		8.34	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2192	12079		1.27	4.0E-16	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2,complete and partial cds
2328	12209	22107	1.32	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2328	12209	22108	1.32	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3411	13328	23129	3.85	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4050	13952	23728	3.55	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4050	13952	23729	3.55	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5092	14962	24737	1	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6538	16396	26575	33.8	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7358	17226	27425	1.22	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
8551	18421	28691	1.74	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTFAWA03 5'
9156	18906		1.64	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9244	18957		5.94	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc6365
9255	18964	25319	2.04	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
128	10102	19924	1.59	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
128	10102	19925	1.59	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
458	10402		1.47	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
467	10410		1.6	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1436	11341	21207	2.01	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2946	12873	22670	4.05	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3874	13785		8.18	3.0E-16	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3876	13786		0.99	3.0E-16	U03887.1	NT	Human BXP20 gene
4861	14741	24521	1.01	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5452	15373	25431	1.41	3.0E-16	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
7031	16908	27098	4.72	3.0E-16	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
7691	17541		1.27	3.0E-16	BF690617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
7828	17678	27922	3.08	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
956	10880		1.18	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2337	12217		0.96	2.0E-16	AA621761.1	EST_HUMAN	af06d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2657	12524		1.71	2.0E-16	J03061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4087	13987	23764	1.33	2.0E-16	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
6646	16526	26720	1.63	2.0E-16	AI732837.1	EST_HUMAN	nz47f06.x5 NCI_CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 ;contains MER7.t1 MER7 repetitive element ;
178	10149	19963	2.55	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
377	10361		22.41	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.t2 OFR repetitive element ;
1928	11823	21704	2.44	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5877	15783		23.72	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
5960	15865	25987	2.81	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6458	15783		6.59	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
7349	17217	27416	1.31	1.0E-16	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
3679	13593	23379	2.54	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6035	15938		2.02	9.0E-17	AI392964.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.t2 MER28 repetitive element ;
6720	16600		4.87	9.0E-17	AW150257.1	EST_HUMAN	xg49g12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.t2 OFR repetitive element ;

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7870	17720		2.18	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1001	10919		1.7	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
3817	13729		0.87	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5427	19444	25402	3.56	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
6311	16174		1.36	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1442	11347		3.18	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (Apobec2), mRNA
5262	15184		3.05	7.0E-17	AF216650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6017	15921	26052	6.83	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
196	10168	19986	4.78	6.0E-17	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
5812	15717	25830	1.61	6.0E-17	AW662772.1	EST_HUMAN	hl81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978695 3' similar to contains L1.t2 L1 repetitive element ;
415	9982	19773	2.31	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 *Stratagene lung* (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
6476	16335	26502	2.07	5.0E-17	T81043.1	EST_HUMAN	yd26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
8783	18598	28887	2.12	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9171	18914		1.98	4.0E-17	AI073546.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA *clone* IMAGE:1640286 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains MER10.t2 MER10 repetitive element ;
2051	11941	21836	1.35	3.0E-17	AW119123.1	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3157	13082		1.31	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3590	13504	23293	1.14	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
3590	13504	23294	1.14	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
7594	17445	27660	4.72	3.0E-17	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9134	18890		3.16	3.0E-17	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
9909	19386		16.82	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLCDIF08 5'
350	10309	20127	2.81	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
351	10309	20127	2	2.0E-17	AI270080.1	EST_HUMAN	qt63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alu repetitive element;
972	10896		1.27	2.0E-17	AA722932.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:399751 3'
2397	12275	22170	2.6	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2397	12275	22171	2.6	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2899	12826	22621	5.62	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5295	15216	25017	1.95	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5295	15216	25018	1.95	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5790	15696		2.07	2.0E-17	AF055066.1	NT	Homo sapiens MHC class 1 region
6711	16591	26779	1.44	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
6925	16803	26997	1.38	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
7699	17549	27772	2.72	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7699	17549	27773	2.72	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7887	17737	27981	5.3	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
733	10665	20499	3.37	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1729	11630	21499	2.45	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2069	11959	21853	1.68	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2287	12170	22067	1.46	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3519	13435		1.01	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4045	13947		7.17	1.0E-17	R09942.1	EST_HUMAN	yf30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
5885	15792		4.7	1.0E-17	AW468468.1	EST_HUMAN	he38e05.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921312 3' similar to contains Alu repetitive element;contains LTR8.t1 LTR8 repetitive element ;
6006	15911	26037	1.44	1.0E-17	AI185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6006	15911	26038	1.44	1.0E-17	AI185642.1	EST_HUMAN	qe65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6216	16082	26232	1.32	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8719	18536	28821	2.01	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2422	12299	22196	0.96	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
7468	17328		3.26	9.0E-18	AI472167.1	EST_HUMAN	tj86d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3718	13630	23415	1.75	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
346	10305	20121	8.39	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
346	10305	20122	8.39	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
5136	15003	24774	0.85	7.0E-18	R16220.1	EST_HUMAN	ya49c07.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53285 3' similar to contains L1 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9638	10305	20121	5.73	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
9638	10305	20122	5.73	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3255	13178	22976	1.16	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4641	14529		3.37	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
6799	16678		2.69	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8476	18349	28614	1.75	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8642	18506	28784	1.78	6.0E-18	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
9394	19052	25308	3.66	6.0E-18	U87929.1	NT	Human aconitate hydratase (ACO2) gene, exon 4
1130	11044	20886	14.74	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
4217	14115	23893	0.92	5.0E-18	10946665	NT	Mus musculus gasdermin (Gsdm), mRNA
6058	14928	24700	1.76	5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
5224	15147	24914	1.38	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
7061	16938	27128	4.26	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221099-002-c06 HT0161 Homo sapiens cDNA
8346	18223	28474	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
8346	18223	28475	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
9512	19125		5.3	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
9837	19336		13	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCCGA02 3'
119	10096	19915	1.36	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
119	10096	19916	1.36	4.0E-18	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
1846	11742		1.08	4.0E-18	AI738592.1	EST_HUMAN	wi33h08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2164	12042	21940	0.98	4.0E-18	Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2154	12042	21941	0.98	4.0E-18	Q06430	SWISSPROT	N-ACETYLLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
5293	15214	25014	2.55	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

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5293	15214	25015	2.55	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8370	18247	28499	7.12	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
831	10758	20609	2.38	3.0E-18	AA814196.1	EST_HUMAN	ob23h11.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN P46782 40S RIBOSOMAL PROTEIN S5. ;
914	10838	20686	2.41	3.0E-18	BE088634.1	EST_HUMAN	CM0-BT0690-210300-298-g07 BT0690 Homo sapiens cDNA
3867	13778	23571	1.19	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6084	16029	26169	5.2	3.0E-18	BE001671.1	EST_HUMAN	PM0-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
9642	19210		4.92	3.0E-18	AW022015.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
251	10217	20034	2.83	2.0E-18	AW836820.1	EST_HUMAN	QV1-LT0036-150200-070-e07 LT0036 Homo sapiens cDNA
1135	11049		47.22	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5322	15242		3.2	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577 O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE. ;
5380	15299	25149	3.04	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5380	15299	25150	3.04	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5585	15500		1.67	2.0E-18	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
5814	15720	25834	3.53	2.0E-18	AW665853.1	EST_HUMAN	hi94g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER19.t2 MER19 repetitive element ;
7779	17629	27861	1.53	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
7779	17629	27862	1.53	2.0E-18	AW151673.1	EST_HUMAN	xf67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.t2 MER10 repetitive element ;
8340	18217	28469	5.32	2.0E-18	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
8968	18774	29065	4.44	2.0E-18	AW151299.1	EST_HUMAN	xg47e09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2 MER8 repetitive element ;
9325	11049		3.15	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4318	14215		1.02	1.0E-18	T95406.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element ;
5286	15208	24985	2.38	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'
5419	15340	25394	1.97	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5419	15340	25395	1.97	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5883	15790	25912	1.32	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7696	17546	27769	4.4	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9277	18980	25324	2.53	1.0E-18	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
533	10475	20289	4.28	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
534	10475	20289	3.19	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
6584	16464		5.21	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
7042	16919	27110	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7042	16919	27111	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8470	18343	28608	3.88	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
9042	10475	20289	8.69	9.0E-19	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
1032	10950		1.54	8.0E-19	AW974902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
2198	12085	21987	1.58	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
5884	15791	25913	2.15	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
9179	19742		2.95	7.0E-19	AA705684.1	EST_HUMAN	zi60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3713	13626		1.02	6.0E-19	AW852930.1	EST_HUMAN	PM0-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4360	14256	24041	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4360	14256	24042	1.36	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4694	14580		1.16	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4952	14829	24595	1.09	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5'
5571	15486	25562	5.24	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8824	18637	28921	7.19	5.0E-19	AW183725.1	EST_HUMAN	xj87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element ;
9849	19495		1.52	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
542	10483	20293	1.45	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2649	12516	22406	1.39	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3778	13690	23476	1.74	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3778	13690	23476	1.74	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4345	14242	24024	1.18	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
6370	16232		2.47	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
7443	16456	26645	1.23	3.0E-19	X89685.1	NT	M.musculus mRNA for TPCR33 protein
9416	19068		7.38	3.0E-19	AF165520.1	NT	Homo sapiens phorbolin I protein (PBI) mRNA, complete cds
2513	12387	22279	17.57	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6849	16728	26923	8.96	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
473	10417		1.6	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2118	12007	21906	1.4	1.0E-19	H30795.1	EST_HUMAN	yo79g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element ;
2686	12550		2.88	1.0E-19	D38044.1	NT	*Human gene for Ah-receptor, exon 7-9*
2817	12746		5.03	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3355	13274	23075	1.27	1.0E-19	AA834967.1	EST_HUMAN	aj49b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.t2 MER37 repetitive element ;
5701	15609	25711	2.37	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, *partial cds*
6919	16797	26990	1.79	1.0E-19	M64657.1	NT	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
7076	16953		2.83	1.0E-19	T99920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element ;
7853	17703	27948	25.21	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
7857	17707	27953	1.79	1.0E-19	N44631.1	EST_HUMAN	yy31e09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272872 5'
6005	15910	26035	2.22	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6005	15910	26036	2.22	8.0E-20	7657286	NT	Mus musculus keratin-associated *protein* 9-1 (Krtap9-1), mRNA
6439	16300	26462	1.31	8.0E-20	AI221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
6439	16300	26463	1.31	8.0E-20	AI221371.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3238	13161	22961	0.88	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
6176	15133	24852	5.53	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D092 5'
6947	16825	27018	10.99	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
6947	16825	27019	10.99	7.0E-20	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
8952	18759		10.45	7.0E-20	6912633	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3508	13424	23227	3.85	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E. Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4175	14075	23850	2.55	6.0E-20	BE622434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4491	14385		1.17	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
6634	16514	26704	4.66	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
6634	16514	26705	4.66	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
7128	17005	27197	1.44	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
7128	17005	27198	1.44	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
6624	16504		6.03	4.0E-20	AI874352.1	EST_HUMAN	tz64g03.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293396 3'
7995	17845	28087	1.17	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2092	11981	21876	1.04	3.0E-20	U03888.1	NT	Human BXP21 gene
4115	14015	23795	1.69	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I14
4524	14417	24201	0.86	3.0E-20	AA037616.1	EST_HUMAN	zk36b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.t3 L1 repetitive element ;
7172	17049		3.26	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
8055	17946		2.08	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9195	18929	25352	5.37	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
813	10741		4.52	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
1095	11011	20852	2.03	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN. ;
1095	11011	20853	2.03	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066 G1224066 ORF2: FUNCTION UNKNOWN. ;
2786	10741		2.72	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
4866	14746	24525	4.32	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4866	14746	24526	4.32	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5090	14960		11.35	2.0E-20	5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
7301	17177	27378	2.95	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
7301	17177	27379	2.95	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8993	18797	29089	1.95	2.0E-20	AA766755.1	EST_HUMAN	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2 MER4 repetitive element ;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8993	18797	29090	1.95	2.0E-20	AA766755.1	EST_HUMAN	oa35b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306935 3' similar to contains MER4.b2 MER4 repetitive element ;
9574	19482	25129	1.5	2.0E-20	H55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
1967	12648	21751	5.25	1.0E-20	AA281961.1	EST_HUMAN	zt11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.t2 MER19 repetitive element ;
4338	14235	24018	1	1.0E-20	BF115158.1	EST_HUMAN	hr84b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.t2 L1 repetitive element ;
7285	17161	27369	2.42	1.0E-20	11418491	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
8839	18652	28940	2.81	1.0E-20	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9321	19011		1.84	1.0E-20	AA420453.1	EST_HUMAN	nc60g08.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.t3 L1 repetitive element ;
2883	12810		1.08	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-8J21
9045	18830		2.35	9.0E-21	AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7116	16992		1.74	8.0E-21	AW674891.1	EST_HUMAN	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN O95169 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
8825	18638	28922	3.42	8.0E-21	AA809411.1	EST_HUMAN	ob71f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
9207	18938		4.02	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2023	11914	21803	2.07	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2023	11914	21804	2.07	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4161	14061		4.96	7.0E-21	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
6887	16766	26962	1.43	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7036	16913	27102	6.84	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
8080	17971	28220	2.94	7.0E-21	AA723404.1	EST_HUMAN	zg73d03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.t3 OFR repetitive element ;
8590	18458	28727	2.37	7.0E-21	7706668	NT	Homo sapiens PTD013 *protein* (PTD013), mRNA
4014	13920	23696	0.94	6.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
907	10831	20678	1.6	5.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
2234	12119	22021	1.08	5.0E-21	AA928194.1	EST_HUMAN	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4266	14165	23942	2.65	5.0E-21	BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4696	14582	24375	5.98	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5109	14977		0.95	5.0E-21	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1701	11602	21473	1.24	4.0E-21	AA970713.1	EST_HUMAN	oo86e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element ;
6106	16000	26138	3.06	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
2228	12113	22015	1.06	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3041	12968	22762	4.04	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5749	15657		1.72	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'
6206	15966	26100	4.79	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
7589	17440	27656	1.55	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
9684	19672	24992	1.32	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
140	10114		14.75	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
919	10843	20688	0.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
919	10843	20689	0.85	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1196	11106		2.09	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
2599	12468	22361	2.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2599	12468	22362	2.89	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5370	15290	25126	1.77	2.0E-21	AI624582.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854 HYPOTHETICAL 51.1 KD PROTEIN ;
6870	16749	26944	4.66	2.0E-21	BE141785.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
7122	16999	27190	3.43	2.0E-21	AU136779.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
8412	18287		1.98	2.0E-21	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8636	18501	28776	1.92	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
8636	18501	28777	1.92	2.0E-21	BE973829.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
9425	19072		5.13	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1235	11142	20994	1.68	1.0E-21	AA557657.1	EST_HUMAN	nl46c04.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element ;
1381	11286		2.46	1.0E-21	AI601264.1	EST_HUMAN	ar88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
5907	15813		2.43	1.0E-21	AL079752.1	EST_HUMAN	DKFZp434I0830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I0830 5'
6269	16134	26289	4.43	1.0E-21	AI223104.1	EST_HUMAN	qg47e05.x1 Soares_testis_NHT Homo:sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 QM PROTEIN (HUMAN);
8021	17871		1.46	1.0E-21	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
4312	14209	23993	2.55	9.0E-22	AI702438.1	EST_HUMAN	tz94a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7002	16879	27070	1.26	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
7002	16879	27071	1.26	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8171	18059	28309	3.65	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
8945	18753	29048	2.92	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
8997	18800		2.39	9.0E-22	9790256	NT	Mus musculus TF-1 cell apoptosis related protein-15 (Tfar15), mRNA
933	10858		4.55	8.0E-22	BE144748.1	EST_HUMAN	CM0-HT0179-281099-076-h05 HT0179 Homo sapiens cDNA
6609	16489		3.8	8.0E-22	AA046502.1	EST_HUMAN	zk67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
649	10585	20401	4.23	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4186	14086	23861	2.32	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4969	14844	24613	1.18	7.0E-22	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7044	16921		1.34	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
7127	17004	27196	2.63	7.0E-22	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
7538	17389	27599	1.86	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
6796	16675		1.82	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5927	15832	25955	2.53	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7912	17762	28001	3.97	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
9645	19213		2.03	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3584	13498		0.85	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
6902	19767		2.7	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8105	17995	28244	2.97	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
9803	19315		1.51	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
943	10868		1.2	3.0E-22	AI469679.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN);contains L1.t1 L1 repetitive element ;
2523	12397	22288	1.86	3.0E-22	AI859038.1	EST_HUMAN	wl66b04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
3620	13534		1.49	3.0E-22	D14718.1	NT	Human chromosomal protein HMG1 related gene
4695	14581	24374	2.72	3.0E-22	AI090125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.t2 MER12 repetitive element ;
6793	16672	26864	2.75	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
1910	11805		2.86	2.0E-22	N24942.1	EST_HUMAN	yx73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2476	12352	22244	1.33	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3373	13292	23091	4.06	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4133	14033	23808	1.26	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5570	19447	25561	1.44	2.0E-22	W39456.1	EST_HUMAN	zo20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
5747	15655	25763	3.39	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
7595	17446	27661	1.49	2.0E-22	AI276522.1	EST_HUMAN	ql76h06.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.t3 MER29 repetitive element ;
7640	17490	27710	7.07	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
7640	17490	27711	7.07	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219269 3'
8974	18779	29071	2.04	2.0E-22	AW418960.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
9009	19304	25200	1.85	2.0E-22	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1836	11733	21609	1.78	1.0E-22	AW865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
2539	12413	22303	2.65	1.0E-22	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
3365	13284	23084	1.74	1.0E-22	D14547.1	NT	Human DNA, SINE repetitive element
6553	16411	26589	1.49	1.0E-22	BE084667.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
9844	19342		4.71	9.0E-23	AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3523	13439	23236	0.84	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
5241	15165	24935	1.48	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
5241	15165	24936	1.48	8.0E-23	AI133716.1	EST_HUMAN	HA2340 Human fetal liver cDNA library Homo sapiens cDNA
3271	13192		1.45	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAWC07 3'
4764	14649	24438	1.04	7.0E-23	10092626	NT	Homo sapiens DKFZP564O0463 protein (DKFZP564O0463), mRNA
8398	18274	28526	3.51	7.0E-23	5031952	NT	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L) mRNA
3387	13305		1.62	6.0E-23	AF199333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4171	14071	23846	3.12	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
9146	18899	25338	1.99	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9146	18899	25339	1.99	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9341	19021	25297	2.18	6.0E-23	AI209130.1	EST_HUMAN	qg59c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MV10_MOUSE P23249 PROTEIN MOV-10. ;
5341	15262	25088	3.51	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
5781	19454	25797	3.51	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6397	19454	25797	3.04	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6580	16460	26653	3.56	3.0E-23	AA130165.1	EST_HUMAN	zl35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.t2 MER29 repetitive element ;
7329	17233	27435	3.61	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
7329	17233	27436	3.61	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
650	10586	20402	4.36	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1126	12644		2.77	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2765	12627	22519	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2765	12627	22520	1.06	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3325	13245		1.46	2.0E-23	AI201458.1	EST_HUMAN	qs73f11.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
3655	13569		3.03	2.0E-23	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3894	13804	23589	2.98	2.0E-23	H59931.1	EST_HUMAN	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3894	13804	23590	2.98	2.0E-23	H59931.1	EST_HUMAN	yr16a02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
6595	16475		5.62	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
9131	18888		2.69	2.0E-23	M32658.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
9656	19218		2.47	2.0E-23	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9774	19676		2.02	2.0E-23	AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4428	14323	24110	1.6	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4657	14543		4.49	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6034	15937		2.91	1.0E-23	BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6865	16744	26937	4.54	1.0E-23	AA448097.1	EST_HUMAN	zw82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.t2 PTR5 repetitive element ;
540	10481		1.88	9.0E-24	AA663213.1	EST_HUMAN	ab75a08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TR:E19822 E19822 CA PROTEIN. ;
4549	14442	24225	1.08	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4549	14442	24226	1.08	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
3796	13708		1.31	7.0E-24	AW937954.1	EST_HUMAN	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
690	10623		2.4	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
820	10748	20595	10.14	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3889	13800	23585	7.18	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
5611	15526	25609	3.06	4.0E-24	AA594178.1	EST_HUMAN	nn31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9506	19121	25293	2.12	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9748	19309	25203	1.53	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
6906	16784		3.02	3.0E-24	AW614871.1	EST_HUMAN	hh68c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2967950 3' similar to contains MER29.b2 MER29 repetitive element ;
7449	17258	27463	4.12	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
9587	19171	25273	5.14	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2298	12180	22078	2.33	2.0E-24	AA167539.1	EST_HUMAN	zp11f09.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3729	13641		1.01	2.0E-24	AW898189.1	EST_HUMAN	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7075	16952	27146	3.14	2.0E-24	AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
9433	19717		6.55	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1670	11572	21438	2.18	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2638	12505		1.87	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
2987	12915	22710	0.91	1.0E-24	D86423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4173	14073		1.63	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6456	16317	26484	4.07	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6633	16513	26703	1.98	1.0E-24	AW901164.1	EST_HUMAN	CM0-NN1010-130300-281-d07 NN1010 Homo sapiens cDNA
4926	14805	24575	2.32	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2 MER1 repetitive element ;
6785	16664	26855	3.75	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
8942	18750	29045	7.46	7.0E-25	AA583540.1	EST_HUMAN	nf25h06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
6174	15131		4.32	6.0E-25	W87623.1	EST_HUMAN	zh65h07.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
6543	16401	26580	11.44	6.0E-25	7305360	NT	Mus musculus otogelin (Otog), mRNA
5166	15032	24799	0.95	5.0E-25	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA
8634	18499	28774	3.61	5.0E-25	AW979107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
1430	11335	21201	2.08	4.0E-25	T98107.1	EST_HUMAN	ye56h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3356	13275		2.78	4.0E-25	AW887671.1	EST_HUMAN	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4221	14119		3.02	4.0E-25	BE170957.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3278	13199	22999	2.66	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3278	13199	23000	2.66	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4798	14683	24470	0.85	3.0E-25	P29622	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6854	16733	26926	2.47	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8394	18270	28522	2.03	3.0E-25	AA579013.1	EST_HUMAN	nf30h10.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.t1 L1 repetitive element ;
1325	11232	21088	3.37	2.0E-25	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2260	12144	22043	7.11	2.0E-25	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2801	12370	22263	4.32	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	13996	23773	1.91	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4096	13996	23774	1.91	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
7629	17480	27700	2.25	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
361	10317	20138	1.61	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
1228	11136		1.21	1.0E-25	9635487	NT	Human endogenous retrovirus, complete genome
2384	12264	22156	2.79	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4753	14638	24425	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
6069	19460	26199	2.85	1.0E-25	AA582690.1	EST_HUMAN	nn54h11.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
6616	16496	26683	3.15	1.0E-25	AA709079.1	EST_HUMAN	zf96g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.t3 PTR5 repetitive element ;
8337	18214	28467	3.5	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
9143	18897	28796	1.45	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9143	18897	28797	1.45	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9914	19389		1.32	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
2433	12310	22206	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
9010	19501		1.73	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5492	15411		1.56	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1559	11464	21321	1.44	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3898	13808	23594	1.35	7.0E-26	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4067	13969	23745	2.03	7.0E-26	AW340153.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908366 3'
8923	18731		7.99	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
9700	19250		1.33	7.0E-26	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGC Homo sapiens cDNA
2178	12065	21967	2.44	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3302	13223	23025	1.42	6.0E-26	AA206131.1	EST_HUMAN	zq52h04.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
8932	18740	29033	4.98	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1160	11073	20918	3.33	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
1160	11073	20919	3.33	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371 ;
9976	19435		1.71	5.0E-26	AI761429.1	EST_HUMAN	wg65e06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2369986 3' similar to contains Alu repetitive element;
1525	11430		1.52	4.0E-26	AA329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
7416	17283		3.77	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
8053	17944	28194	3.74	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1958	11853	21740	1.5	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434I066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I066 5'
1987	11880		2.41	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3712	13625	23408	1.19	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
3712	13625	23409	1.19	3.0E-26	AA152464.1	EST_HUMAN	zo30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
6131	15978	26114	4.35	3.0E-26	BF245458.1	EST_HUMAN	601864963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
8108	17998		2.18	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
8853	18665	28951	1.99	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8853	18665	28952	1.99	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8879	18691	28984	10.55	3.0E-26	AA583173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.t1 OFR repetitive element ;
666	10600	20418	5.61	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1825	11722		3.36	2.0E-26	AL038099.2	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3193	13118	22924	4.26	2.0E-26	X86694.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
8135	18023		2.88	2.0E-26	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8549	18420	28690	4.55	2.0E-26	AI801412.1	EST_HUMAN	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element;contains element MER20 MER20 repetitive element ;
8720	18537		1.82	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
9252	18962		2.19	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
132	10106	19927	2.36	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2001	11894	21786	1.39	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2516	12390	22282	0.84	1.0E-26	BE814995.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2654	12521		16.79	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6089	16034		2.75	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8266	18146		3.17	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
9493	19737		1.84	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
7364	17342		3.11	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
8027	19470	28118	3.48	9.0E-27	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
9013	18812		3.97	9.0E-27	BF445556.1	EST_HUMAN	naa03c07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.t1 OFR repetitive element ;
10	9996	19787	3.09	8.0E-27	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
545	10486		4.13	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1395	11300	21158	18.87	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1395	11300	21159	18.87	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
2121	12009	21909	0.98	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
3148	13073	22874	3.31	8.0E-27	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3309	13230	23035	0.91	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
6165	15122		3.12	8.0E-27	BE926560.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
6196	15956	26088	4	8.0E-27	N84970.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
7310	17186	27386	1.68	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
7310	17186	27387	1.68	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
668	10602		1.22	7.0E-27	Z70664.1	NT	Human endogenous retroviral element HC2
5023	14896		2.09	7.0E-27	AW629172.1	EST_HUMAN	hi51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
8132	18020		4.22	7.0E-27	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
9631	19204		2.07	7.0E-27	AV723365.1	EST_HUMAN	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
8109	17999	28246	6.21	6.0E-27	M26697.1	NT	Human nucleolar protein (B23) mRNA, complete cds
7877	17727	27970	2.92	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
7877	17727	27971	2.92	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6046	15949	26080	1.54	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6656	16536		1.23	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8880	18692	28985	2.56	4.0E-27	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1995	11889	21782	5.42	3.0E-27	X60658.1	NT	R.rattus RYA3 mRNA for a potential ligand-binding protein
4174	14074	23849	1.27	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
5278	15200	24976	5.13	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
7365	17343	27549	2.98	3.0E-27	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
36	10023	19820	7.96	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1853	11749		18.58	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3071	12998		10.27	2.0E-27	AW629172.1	EST_HUMAN	hl51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
3187	13112	22916	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3187	13112	22917	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3944	13852	23627	1.09	2.0E-27	AF000368.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6712	16592	26780	1.5	2.0E-27	AI866347.1	EST_HUMAN	wl28g07.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426268 3'
7338	17206		2.3	2.0E-27	AA551527.1	EST_HUMAN	nh08h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1 repetitive element ;
7768	17618	27847	1.22	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
7768	17618	27848	1.22	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07
8324	18201	28450	2.89	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
8778	11749		20.82	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
429	10374		1.56	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
980	10903	20749	1.41	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5943	15848	25972	6.31	1.0E-27	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6105	15999	26136	2.2	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6105	15999	26137	2.2	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
7005	16882	27075	1.72	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7194	17071		1.89	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
7606	17457	27672	2.68	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
8943	18751	29046	3.14	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
136	10109		2.32	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313 ;
308	10270	20089	3.01	9.0E-28	AU126260.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
5118	14986	24760	1.21	9.0E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ;
5118	14986	24761	1.21	9.0E-28	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ;
9093	18866		3.74	9.0E-28	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
9418	19592		1.97	8.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN. ;contains element MER22 repetitive element ;
1164	11077	20922	7.54	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
8523	18395	28660	2.54	7.0E-28	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9053	18836		1.44	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
3987	13894	23670	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
3987	13894	23671	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
9673	19232		2.73	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element;contains element PTR5 repetitive element ;
315	10277		3.08	5.0E-28	AI921003.1	EST_HUMAN	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element ;
3927	13836	23616	1.85	5.0E-28	R79762.1	EST_HUMAN	yi89f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
2584	12465	22347	1.42	4.0E-28	AW195066.1	EST_HUMAN	xn33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
3070	12997	22788	3.39	4.0E-28	BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636305 5'
6336	16199	26359	1.59	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
8239	18119		4.29	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
8371	18248		53.6	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
8388	16199	26359	2.94	4.0E-28	AI198941.1	EST_HUMAN	qf66f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
1262	11169		1.89	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
7124	17001	27183	2.19	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-f09 HT0713 Homo sapiens cDNA
8306	18183	28430	1.84	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9489	19106		2.44	3.0E-28	AI831991.1	EST_HUMAN	wj98f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element;contains element HGR repetitive element ;
83	10067	19884	6.45	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1149	11062	20905	10	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2427	12304	22200	2.1	2.0E-28	AI348634.1	EST_HUMAN	qo35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element ;
5821	15727		4.28	2.0E-28	BF212905.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
7528	17379		5.86	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
8887	18698	28992	2.27	2.0E-28	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1463	11368	21233	2.42	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2173	12060	21963	1.55	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
2650	12517	22407	1.03	1.0E-28	AF000995.1	NT	Homo sapiens ubiquitous TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
6587	16467		4.48	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
6675	16555		3.02	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
7346	17214	27413	2.63	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
7678	17528	27753	5.15	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7678	17528	27754	5.15	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9058	18840		3.95	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
9797	19485		1.43	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9892	19691	24896	2.6	9.0E-29	AW663987.1	EST_HUMAN	hi76g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
9585	19169		2.92	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1584	11488	21349	0.91	7.0E-29	AW966447.1	EST_HUMAN	EST378521 MAGE resequences, MAGI Homo sapiens cDNA
9942	19410		5.08	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
580	10518	20325	6.52	6.0E-29	AI936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;
9353	19028		3.88	6.0E-29	BE940436.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
9438	19076		1.86	6.0E-29	BF568097.1	EST_HUMAN	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 5'
4928	14807		0.98	5.0E-29	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7068	16945		7.61	5.0E-29	AW887541.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3194	13119		1.68	4.0E-29	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5656	15568		6.65	4.0E-29	BE164930.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7079	16956	27149	4.71	4.0E-29	J04988.1	NT	Human 90 kD heat shock protein gene, complete cds
4317	14214	23997	1.45	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
4626	14514	24305	1.31	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
7070	16947	27138	2.07	3.0E-29	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
7362	17229	27429	1.6	3.0E-29	AW303317.1	EST_HUMAN	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.t2 MER19 repetitive element ;
7492	17362		1.64	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8591	18459	28728	2.22	3.0E-29	AA403053.1	EST_HUMAN	zt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;
9248	18959		1.51	3.0E-29	D63882.1	NT	Human HsLIM15 mRNA for HsLim15, complete cds
484	10427	20240	1.43	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
484	10427	20241	1.43	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1516	11421	21278	6.12	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1516	11421	21279	6.12	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4182	14082	23855	2.03	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5750	15658	25765	1.43	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
6461	15658	25765	1.43	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7474	17334	27539	2.95	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7474	17334	27540	2.95	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7879	17729	27973	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7879	17729	27974	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8804	18618		1.96	2.0E-29	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
9004	18807		1.73	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7105	16982	27174	5.41	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
5966	15871	25995	3.04	9.0E-30	AA761215.1	EST_HUMAN	nz20c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element ;
9132	18889		1.5	9.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRTL), mRNA
5815	15721		8.81	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain'cDNA Homo sapiens cDNA clone c-23f05
6812	16691	26880	3.37	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
7039	16916	27105	3.53	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1499	11403		1.16	7.0E-30	BE091133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1549	11454		0.95	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
1736	11637	21505	1.26	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	13078	22878	2.41	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-290400-214-f12 BN0147 Homo sapiens cDNA
9915	11454		3.15	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3931	13840	23620	31.23	5.0E-30	AI399992.1	EST_HUMAN	tg92g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5205	19522		7.35	5.0E-30	U87931.1	NT	Human aconitate hydratase (ACO2) gene, exon 7
8261	18141		3.55	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8495	18368	28632	6.68	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8495	18368	28633	6.68	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2096	11985	21880	1.64	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2096	11985	21881	1.64	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
7162	17039	27231	1.49	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1134	11048		1.71	3.0E-30	AI338551.1	EST_HUMAN	qq93c05.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element ;
3697	13611	23395	0.91	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8538	18410	28675	2.38	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
659	10593	20411	1.18	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1068	10984		2.32	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1464	11369	21234	5.91	2.0E-30	BE175877.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2683	12548	22438	10.97	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2889	12816	22609	6.38	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3721	13633	23419	2.11	2.0E-30	AW206581.1	EST_HUMAN	UI-H-BI1-afo-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4668	14554	24346	1.72	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4668	14554	24347	1.72	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
6966	16844	27036	3.46	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
7019	16896	27085	1.55	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
7019	16896	27086	1.55	2.0E-30	BE670617.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
7743	17593	27814	3.3	2.0E-30	AW971568.1	EST_HUMAN	EST383657 MAGE resequences, MAGL Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7802	17652	27889	4.47	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
284	10249	20069	10.22	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-570C01 5'
527	10469	20281	1.6	1.0E-30	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;
699	10632	20457	2.92	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2165	12052	21953	3.24	1.0E-30	AA664377.1	EST-HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2413	12290	22187	2.57	1.0E-30	BF347728.1	EST_HUMAN	602022560F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157991 5'
2973	12900	22699	1.03	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase; eIF-2-associated p67 (MNPEP), mRNA
3015	12943	22736	0.93	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end
6545	16403	26582	2.32	1.0E-30	BF183230.1	EST_HUMAN	601809932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
9733	19615		5.1	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
7013	16890		2.04	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
1060	10977	20820	1.64	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2362	12242		5.14	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
694	10627		1.72	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2633	12500	22392	1.7	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2633	12500	22393	1.7	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
9583	19168	25272	2.56	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3625	13539		2.79	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6739	16618		3.68	6.0E-31	AF055066.1	NT	Homo sapiens MHC class 1 region
8120	18008	28255	2.11	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'.
9191	18926	25351	1.88	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
9319	19541		1.78	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
185	10157	19973	2.85	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
185	10157	19974	2.85	5.0E-31	M60694.1	NT	*Homo sapiens type I DNA topoisomerase gene, exon 8*
6915	16793		1.21	5.0E-31	BF056540.1	EST_HUMAN	7k06f04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT. ;contains L1.t1 L1 repetitive element ;
581	10519		3.78	4.0E-31	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1594	11498	21357	1.04	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1775	11674		2.59	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2759	12621		1.38	4.0E-31	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
9604	19186		1.52	4.0E-31	11430273	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
9718	19259		1.38	4.0E-31	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2550	12423	22314	1.42	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
6341	16204	26366	9.03	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASHI) (NDUFB8) mRNA
6425	16286	26448	1.38	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
6745	16624		1.95	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7525	17376	27585	2.86	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
8028	17920	28167	2.01	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
8493	18366		6.36	3.0E-31	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1875	11771	21647	1.83	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-f03 LT0051 Homo sapiens cDNA
2167	12054	21955	1.31	2.0E-31	AI393388.1	EST_HUMAN	tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2292	12174	22074	2.18	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2391	12269	22164	4.4	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element ;
5502	15421	25483	3.6	2.0E-31	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
7246	17123		1.8	2.0E-31	AA877764.1	EST_HUMAN	nr06f04.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7309	17185	27385	3.99	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
7700	17550	27774	1.27	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
7700	17550	27775	1.27	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
7797	17647	27883	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
7797	17647	27884	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9292	18993		2	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
9431	19759		1.81	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
16	10002	19794	8.34	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1640	11544	21403	2	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1640	11544	21404	2	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1640	11544	21405	2	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4535	14428	24209	1.01	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547B235 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4535	14428	24210	1.01	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547B235 5'
5235	15159	24927	3.15	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
5728	15635	25738	1.87	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite ceb1 repeat region
8288	18167	28411	2.72	1.0E-31	AI086434.1	EST_HUMAN	qf21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595 Q16595 FRATAXIN. ;
2835	12763		0.99	9.0E-32	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
6000	15905	26029	2.34	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
2032	11923	21815	3.32	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4754	14639	24426	1.17	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
9268	18972		2.77	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K)I gene, part. with 5' breakpoint between orphon and neighbouring non-amplified region
2702	12566	22456	0.9	6.0E-32	AI478104.1	EST_HUMAN	tm34a10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.t3 MER29 repetitive element ;
6359	16222		1.5	6.0E-32	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1018	10936	20779	29.57	5.0E-32	AF116627.1	NT	Homo sapiens PRO1181 mRNA, complete cds
916	10839		1.74	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6484	16342	26510	2.82	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6484	16342	26511	2.82	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
448	10392	20213	3.4	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1438	11343	21210	7.67	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAKC07 5'
7404	17271	27477	6.73	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
7404	17271	27478	6.73	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
8297	18176	28421	8.08	3.0E-32	AA777621.1	EST_HUMAN	zi95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.t3 THR repetitive element ;
9294	18995		3.04	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
9655	15090	24882	2.43	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9655	15090	24883	2.43	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9802	19314		4.94	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4783	14667	24454	0.91	2.0E-32	BE296613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
5900	15806	25929	19.01	2.0E-32	Z38133.1	NT	H.sapiens mRNA for myosin
5900	15806	25930	19.01	2.0E-32	Z38133.1	NT	H.sapiens mRNA for myosin

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6815	16694	26884	3.41	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
6815	16694	26885	3.41	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
9908	19385	25175	1.61	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
9908	19385	25176	1.61	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3055	12982		1.06	1.0E-32	BE743299.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6198	15958	26090	7.04	1.0E-32	11439789	NT	Homo sapiens chromosome 11open reading frame 9 (C11ORF9), mRNA
6997	16874	27065	5.18	1.0E-32	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
3435	13352		4.98	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11. ;
5867	15773		4.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7103	16980	27172	1.99	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
8177	18065		5.89	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
54	10041	19850	2.06	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
54	10041	19851	2.06	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2115	12004	21902	2.71	7.0E-33	AI590115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.t1 OFR repetitive element ;
2612	12480		8.4	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
2800	11573	21439	1.78	7.0E-33	AV730015.1	EST_HUMAN	AV730015 HTF Homo sapiens cDNA clone HTFANF08 5'
3204	13128		12.85	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGE resequences, MAGL Homo sapiens cDNA
8203	18087	28338	3.9	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
8573	18441	28709	2.15	7.0E-33	AW971568.1	EST_HUMAN	EST383657 MAGE resequences, MAGL Homo sapiens cDNA
9274	18978	25322	3.43	7.0E-33	AA601416.1	EST_HUMAN	no16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.t1 L1 repetitive element ;
3676	13590		0.85	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6988	16865	27059	13.52	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
7049	16926	27117	2.57	6.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
7750	17600	27822	1.24	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
7750	17600	27823	1.24	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1739	11640		1.78	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-a02 FT0169 Homo sapiens cDNA
1838	11735		1.18	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1856	11752	21626	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1856	11752	21627	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2226	12111		1.3	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9082	18858		1.62	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1112	11027		3.28	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2078	11968	21861	1.77	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2370	12250		7.39	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element;contains MER28.b2 MER28 repetitive element ;
2498	12373	22265	3.77	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4382	14278	24057	1.63	4.0E-33	AW293349.1	EST_HUMAN	UI-H-BI2-ahl-c-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5318	15239	25043	20.94	4.0E-33	AA053053.1	EST_HUMAN	zl71a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
9007	18810	29102	1.72	4.0E-33	11425635	NT	Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1), mRNA
1073	10989		4.46	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
1074	10989		3.4	3.0E-33	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2400	12721		1.48	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'
99	10003		2.33	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
4322	14219		4.27	2.0E-33	BE159039.1	EST_HUMAN	MR0-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
4911	14790	24565	5.1	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5026	14899	24668	1.73	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5026	14899	24669	1.73	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5869	15775	25894	1.61	2.0E-33	AI277492.1	EST_HUMAN	ql96d01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
7261	17138		1.8	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1676973 3' similar to gb:M29536 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
8	9994		1.44	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8637	18502	28778	2.02	1.0E-33	AW996818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
8921	18729	29024	5.33	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
9553	19151		1.92	1.0E-33	AI927191.1	EST_HUMAN	wo88c06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9723	9994		3.04	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9754	19278	25229	1.34	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
9927	19399		2.09	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
1427	11332	21198	1.98	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
9340	19020		3.08	7.0E-34	H12866.1	EST_HUMAN	yj14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
463	10406	20225	1.46	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
463	10406	20226	1.46	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
9153	18903	25340	1.44	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hacl-1) gene
1837	11734		2.23	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
4993	14868	24631	4	5.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds
7144	17021	27215	1.18	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8046	17937	28186	2.12	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
8578	18446		2.01	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1953	11848	21735	2.11	4.0E-34	AI804667.1	EST_HUMAN	tt94c06.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2249194 3'
2687	12552	22441	0.98	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
8492	18365		4.81	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1488	11393	21254	8.56	1.0E-34	P12236	SWISSPROT	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3621	13535	23320	1.46	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3979	13886	23661	0.78	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
3979	13886	23662	0.78	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4381	14277		4.02	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-h08 BT0506 Homo sapiens cDNA
4920	14799		0.86	1.0E-34	AW845706.1	EST_HUMAN	MR0-CT0068-280999-002-d11 CT0068 Homo sapiens cDNA
5731	15639	25743	1.99	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
5731	15639	25744	1.99	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
7155	17032	27226	3.87	1.0E-34	AW368451.1	EST_HUMAN	CM4-HT0193-061099-022-g06 HT0193 Homo sapiens cDNA
7591	17442	27658	8.89	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564A1563 5'
9746	19307		2.92	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3594	13508	23296	1.26	9.0E-35	AW663302.1	EST_HUMAN	hh77b06.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
219	10189		24.25	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1703	11604	21475	3.3	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA. ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1703	11604	21476	3.3	8.0E-35	BF589937.1	EST_HUMAN	naa33a08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA. ;
4761	14646	24435	3.09	8.0E-35	BF183195.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
8075	17966	28217	3	8.0E-35	BE378480.1	EST_HUMAN	601236468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
9265	18969		3.49	8.0E-35	BF569282.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300660 3'
5905	15811	25937	1.52	7.0E-35	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1391	11296	21154	1.28	6.0E-35	AA757115.1	EST_HUMAN	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1309397 3'
1926	11820	21699	1.78	6.0E-35	6005975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
6610	16490	26676	3.6	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7698	17548	27771	2.7	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
1681	11583	21454	2.29	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
4311	14208	23992	2.2	5.0E-35	AF023268.1	NT	Homo sapiens clk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
6761	16640		3.14	5.0E-35	BE890992.1	EST_HUMAN	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
6779	16658	26848	2.18	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
6779	16658	26849	2.18	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8517	18389		3.42	5.0E-35	AA001786.1	EST_HUMAN	zh84f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1415	11321	21186	14.91	4.0E-35	BE257907.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1776	11675	21552	5.1	4.0E-35	H91193.1	EST_HUMAN	yu98a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
5042	14914		1.29	4.0E-35	BE409102.1	EST_HUMAN	601300705F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
6280	16144		1.82	4.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
6957	16835	27030	6.84	4.0E-35	AL046596.1	EST_HUMAN	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1561	11466	21324	9.63	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
2283	12167		2.42	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
4793	14678	24465	1.06	3.0E-35	BF376402.1	EST_HUMAN	MR1-TN0045-130900-010-e01 TN0045 Homo sapiens cDNA
5275	15197	24971	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;
5275	15197	24972	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q9QZH7 F-BOX PROTEIN FBL2. ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7465	17325		1.81	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
103	12659	19902	1.74	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
1171	11083	20928	1.25	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2171	12058	21961	5.2	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
3272	13193	22991	0.97	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3272	13193	22992	0.97	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3511	13427		0.88	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3835	13747	23539	1.09	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3835	13747	23540	1.09	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4570	14462		2.55	2.0E-35	H49239.1	EST_HUMAN	yq19a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:274079 5'
5426	15347	25401	1.66	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
8175	18063	28312	3.72	2.0E-35	X59417.1	NT	H.sapiens PROS-27 mRNA
9028	13193	22991	1.36	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
9028	13193	22992	1.36	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
9205	18936	25354	1.51	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
9205	18936	25355	1.51	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
9725	19264		3.97	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9832	12659	19902	4.17	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
40	10028	19828	4.38	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
40	10028	19829	4.38	1.0E-35	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	10667	20500	44.43	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
735	10667	20501	44.43	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
891	10817		1.16	1.0E-35	T87947.1	EST_HUMAN	yd93a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2495	12369	22262	2.31	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2740	12602	22496	1.11	1.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2740	12602	22497	1.11	1.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3104	13030	22826	1.07	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
3126	13051	22848	2.2	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'
3126	13051	22849	2.2	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF06 3'
4325	14222	24003	4.7	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4325	14222	24004	4.7	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5382	15301	25154	1.43	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7501	19469	27578	2	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
7501	19469	27579	2	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
8977	18782		4.16	1.0E-35	AI525119.1	EST_HUMAN	promrna-7.D01.r bvtumor Homo sapiens cDNA 5'
9186	12369	22262	1.69	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
9267	18971		1.37	1.0E-35	11418110	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
9620	19198		2.26	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
2900	12827	22622	0.94	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
3080	13007		4.03	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
6512	16371	26548	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
6512	16371	26549	6.04	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and L/N
9423	19071	25279	5.23	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
1959	11854	21741	1.88	6.0E-36	7706622	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2367	12247		6.17	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3587	13501	23290	0.91	6.0E-36	BF515101.1	EST_HUMAN	UI-H-BW1-anv-c-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5268	15190	24965	19.79	6.0E-36	AI435169.1	EST_HUMAN	th93b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
6221	16087	26237	3.34	6.0E-36	AW780143.1	EST_HUMAN	ho06h02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN P52292 IMPORTIN ALPHA-2 SUBUNIT ;
7027	16904	27096	2.21	6.0E-36	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
8833	18646	28931	2.74	6.0E-36	AI380499.1	EST_HUMAN	tf95c09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2 MER9 repetitive element ;
9821	19580	25071	1.69	6.0E-36	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
133	10107	19928	6.69	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2722	12584	22478	7.71	5.0E-36	BE388436.1	EST_HUMAN	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3561	13475	23264	1.96	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4678	14564	24358	1.42	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4678	14564	24359	1.42	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
9026	10107	19928	2.64	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9318	19010	25337	2.36	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1205	11115	20961	1.43	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1424	11329	21196	1.54	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1626	11530	21389	1.58	4.0E-36	BE382574.1	EST_HUMAN	601298574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
2175	12062		1.63	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3310	13231	23036	3.21	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3310	13231	23037	3.21	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5693	15602	25704	2.21	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), trancript variant 3, mRNA
6511	16370	26547	1.74	4.0E-36	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
6979	16856	27050	1.41	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6979	16856	27051	1.41	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8356	18233	28481	2.19	4.0E-36	AA400370.1	EST_HUMAN	zu69c10.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
9334	19015		1.31	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9380	19545		2.85	4.0E-36	AV753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
681	10614	20437	2.73	3.0E-36	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
2252	12136	22033	0.89	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4402	14297	24081	5.15	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
8452	18325	28584	1.78	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3132	13057	22857	2.7	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
4877	14757	24534	4.62	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5371	15291	25127	2.16	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
5567	15483	25556	3.99	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBJ28 5' end
5962	15867	25989	11.82	2.0E-36	T69629.1	EST_HUMAN	yc44a07.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
867	10793	20643	1.9	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2098	11987	21884	0.86	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2098	11987	21885	0.86	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131199-021-h07 HT0217 Homo sapiens cDNA
2155	12043	21942	1.31	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
5752	15660		5.94	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6640	16520	26711	2.03	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
6640	16520	26712	2.03	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7220	17097	27287	2.84	1.0E-36	AW103658.1	EST_HUMAN	xe82b07.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2614357 3'
7824	17674	27917	4.06	1.0E-36	BF364169.1	EST_HUMAN	QV3-NN1023-010600-199-h01 NN1023 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8317	18194	28444	3.43	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
8686	18574	28857	3.91	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BN0-ale-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
9203	18934		3.74	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9374	19040	25305	1.29	1.0E-36	11418121	NT	Homo sapiens chromosome 22 open reading frame 2 (C22ORF2), mRNA
9647	19214		3.07	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
9890	19371		2.89	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6368	16231	26390	1.96	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
6368	16231	26391	1.96	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
9462	19093		2.79	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
5143	15010	*24781*	1.38	8.0E-37	AB020684.1	NT	*Homo sapiens mRNA for KIAA0877 protein, partial cds*
5213	15136		1.7	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5559	15475	25547	4.1	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
5559	15475	25548	4.1	8.0E-37	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
5584	15499	25576	5.63	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
6602	16482	26670	6.25	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1263	11170		2.51	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
8140	18028	28274	6.77	7.0E-37	AI817700.1	EST_HUMAN	wk25b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.t2 PTR5 repetitive element ;
8268	18148	28388	4.16	7.0E-37	AI536702.1	EST_HUMAN	tm87g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element ;
9775	19292		2.48	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
5707	15615	25716	3.37	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5707	15615	25717	3.37	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8292	18171		4.17	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
9198	18931		3.57	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2374	12254	22145	2.23	4.0E-37	AA702794.1	EST_HUMAN	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
5160	15027		1.11	4.0E-37	N62051.1	EST_HUMAN	EST52g10 WATM1 Homo sapiens cDNA clone 52g10 similar to human STS G04101
1970	11863	21755	2.85	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
1970	11863	21756	2.85	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2465	12341		1.7	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA
2936	12863		3.02	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1064	10980	20824	1.94	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1064	10980	20825	1.94	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1921	11816	21695	1.47	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3818	13730	23519	5.05	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
6007	15912	26039	3.36	2.0E-37	AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
6685	16565	26759	3.23	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
8845	18657	28945	16.4	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
9933	19403		3.15	2.0E-37	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2041	11932	21828	3.61	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3878	13789	23577	22.51	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4072	13974	23753	0.96	1.0E-37	BE872365.1	EST_HUMAN	601448619F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852652 5'
4857	14737	24517	2.13	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
7072	16949	27141	2.85	1.0E-37	AA171406.1	EST_HUMAN	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.t2 L1 repetitive element ;
8082	17973	28222	20.59	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
9508	19122		2.46	1.0E-37	BE771814.1	EST_HUMAN	CM3-FT0096-140700-243-d07 FT0096 Homo sapiens cDNA
5530	15447	25514	3.05	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1203	11113	20959	1.95	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2449	12326	22225	1.44	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4163992 5'
9568	11113	20959	1.36	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2135	12023	21920	1.38	7.0E-38	AW972825.1	EST_HUMAN	EST384920 MAGE resequences, MAGL Homo sapiens cDNA
3005	12933	22726	1.76	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
5432	15352	25407	1.69	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5432	15352	25408	1.69	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
9060	18842		4.46	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
9542	19143	25266	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
710	10642	20468	1.15	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2404	12281	22178	1.79	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
6191	16076	26225	2.42	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074 5'
113	10092	19909	2.56	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
113	10092	19910	2.56	4.0E-38	Z25466.1	NT	B.taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1141	11055	20897	0.82	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2053	11943		4.39	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3638	13552		1.11	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
3781	13693	23480	1.65	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3781	13693	23481	1.65	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4513	14406		0.85	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6050	19459	26083	7.17	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6478	16337	26504	7.64	3.0E-38	BF373664.1	EST_HUMAN	CM3-FT0181-140700-241-f07 FT0181 Homo sapiens cDNA
7025	16902	27094	1.78	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
7025	16902	27095	1.78	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
7727	17577		1.58	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
44	10032	19836	1.41	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	11264	21120	2.6	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
1627	11531	21390	1.66	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1627	11531	21391	1.66	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
6941	16819		4.7	2.0E-38	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
7316	17192		1.47	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710 GAG POLYPROTEIN. ;
7970	17820	28063	1.66	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8781	18596	28885	5.24	2.0E-38	BE712790.1	EST_HUMAN	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
8907	18715	29008	3.69	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
8907	18715	29009	3.69	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
9112	18876		4.05	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAXH07 5'
9115	18878		2	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
9412	19064	25313	3.86	2.0E-38	H55641.1	EST_HUMAN	CHR220680 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
9472	19099		2.26	2.0E-38	S74906.1	NT	E1 beta=pyruvate dehydrogenase beta {promoter} [human, placenta, Genomic, 1280 nt]
9924	19396		2.56	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1077	10993		2.29	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element MER19 repetitive element ;
1954	11849	21736	0.94	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1973	11866	21758	1	1.0E-38	7661969	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2445	12322	22221	1.58	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4063	13965	23743	1.41	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4223	14121	23896	0.83	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4229	14127	23902	1.31	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4229	14127	23903	1.31	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4493	14387	24173	1.21	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5673	15582	25682	3.61	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
5673	15582	25683	3.61	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
6378	16240	26400	2.78	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
7414	17281	27489	6.23	1.0E-38	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
9264	19481		2.33	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
48	10036	19842	5.14	8.0E-39	4502312	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1372	11278	21134	1.51	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1788	11686		1.06	8.0E-39	AI823404.1	EST_HUMAN	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890 POL PROTEIN ;
2047	11938	21832	5.54	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8184	18070	28319	2.12	6.0E-39	BF331829.1	EST_HUMAN	QV1-BT0631-040900-357-f02 BT0631 Homo sapiens cDNA
9838	19337		2.23	6.0E-39	BE670394.1	EST_HUMAN	7e34c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828 ;
991	10912	20757	1.3	6.0E-39	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2957	12884	22682	5.13	5.0E-39	AI750154.1	EST_HUMAN	at36b04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.t1 LTR7 repetitive element ;
9556	19154		1.54	5.0E-39	11420289	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
538	10479	20291	10.53	4.0E-39	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3525	13441	23238	0.96	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6707	16587	26775	1.49	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element ;
9575	19164		3.08	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9687	19240		2.03	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260600-278-c06 FN0063 Homo sapiens cDNA
41	10029	19830	11.27	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
41	10029	19831	11.27	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
41	10029	19832	11.27	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
9104	18871	28781	5.51	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
9104	18871	28782	5.51	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
9147	18900		4.42	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190954 3'
879	10805		4.03	2.0E-39	BE409203.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
894	10820		17.44	2.0E-39	AI525119.1	EST_HUMAN	promrna-7.D01.r bvtumor Homo sapiens cDNA 5'
1015	10933		3.61	2.0E-39	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1513	11418		10.15	2.0E-39	AW372318.1	EST_HUMAN	PM0-BT0340-211299-003-d02 BT0340 Homo sapiens cDNA
1930	11825	21707	10.03	2.0E-39	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
2587	12458	22349	1.75	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4303	14201	23985	1.36	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-280700-011-a10 FN0037 Homo sapiens cDNA
5375	15295	25142	3.4	2.0E-39	AA508880.1	EST_HUMAN	ng86f03.s1 NCI_CGAP_Pr6 Homo sapiens cDNA clone IMAGE:941693
6360	16223	26384	2.17	2.0E-39	AA080867.1	EST_HUMAN	zn06f02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
8731	18587	28874	2.33	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
9922	19394		2.31	2.0E-39	11425464	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1497	11401	21261	1.78	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1497	11401	21262	1.78	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1514	11419	21275	4.95	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4561	14453	24239	5.49	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4561	14453	24240	5.49	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4604	14492	24279	8.58	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5459	15379	25439	1.54	1.0E-39	T80876.1	EST_HUMAN	yd26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element;contains LTR1 repetitive element ;
5476	15395	25460	4.36	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5475	15395	25461	4.36	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6083	16028		1.66	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6357	16220	26382	1.75	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
543	10484	20294	1.67	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1215	11123	20971	10.19	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1216	11123	20972	10.19	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No. .	Top Hit Database Source	Top Hit Descriptor
1433	11338	21205	5.04	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3892	15069	23586	3.58	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4250	14149	23923	0.82	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4398	14149	23923	1.12	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3004	12932	22725	0.95	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3847	13758		2.41	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619166 5'
6541	16399	26578	1.56	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
6541	16399	26579	1.56	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8270	18150	28391	2.83	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2696	12560	22449	3.88	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2696	12560	22450	3.88	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
5616	15531		2.07	6.0E-40	BE504766.1	EST_HUMAN	hz40g01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6141	15989	26124	3.08	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6141	15989	26125	3.08	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7731	17581	27804	6.82	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
7731	17581	27805	6.82	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2561	12433	22326	1.89	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1834	11731	21607	1.38	4.0E-40	AI686005.1	EST_HUMAN	tt91b01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN. ;
2061	11951		2.67	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4291	14189	23973	7.85	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
6662	16542	26738	3.76	4.0E-40	AA742809.1	EST_HUMAN	nv34e10.r1 NCI_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
7237	17114	27308	4.87	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
7237	17114	27309	4.87	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8099	17989	28238	4.07	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4040	13943	23721	0.98	3.0E-40	AI925949.1	EST_HUMAN	wh12f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6001	15906	26030	6.25	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6882	16761	26959	4.28	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7186	17063	27253	1.49	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
7312	17188	27389	1.52	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8387	18264	28515	1.93	3.0E-40	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
8588	18456	28725	11.23	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
8855	18667	28954	1.96	3.0E-40	AW118799.1	EST_HUMAN	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804 Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERVS ;
322	10283		12.69	2.0E-40	AI223036.1	EST_HUMAN	qg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
777	10707		2.72	2.0E-40	AW303868.1	EST_HUMAN	xr24e10.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE P97461 40S RIBOSOMAL PROTEIN S5. ;
1783	11681		1.4	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1892	11787	21664	2.19	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1892	11787	21665	2.19	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2026	11917	21807	1.08	2.0E-40	AI968562.1	EST_HUMAN	wt90a11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929 ZINC FINGER PROTEIN. ;
2123	12011	21910	2.61	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
2333	12214	22112	2.35	2.0E-40	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
2658	12525		1.08	2.0E-40	BE275932.1	EST_HUMAN	601121567F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
3087	13014	22806	3.59	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
4807	14691	24478	1.49	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4807	14691	24479	1.49	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
865	10791		1.65	1.0E-40	AA225989.1	EST_HUMAN	nc09a09.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007608
2580	12451	22343	1.91	1.0E-40	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
2653	12520		1.92	1.0E-40	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
2707	12570	22460	0.92	1.0E-40	BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
2707	12570	22461	0.92	1.0E-40	BF541030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4067736 5'
3258	13181		1.81	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4505	14398	24184	6.28	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
4892	14772	24550	0.88	1.0E-40	7705778	NT	Homo sapiens CGI-65 protein (LOC51103), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6215	16081	26230	2.03	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
6215	16081	26231	2.03	1.0E-40	AA573201.1	EST_HUMAN	nj42f04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
8289	18168	28412	5.72	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
8355	18232	28480	53.3	1.0E-40	AI239572.1	EST_HUMAN	qh31h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846339 3'
9521	19622		3.93	1.0E-40	BF334112.1	EST_HUMAN	MR2-CT0222-211099-002-e10 CT0222 Homo sapiens cDNA
6621	16501	26689	1.73	8.0E-41	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
811	12678	20585	2.36	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
811	12678	20586	2.36	7.0E-41	AI934364.1	EST_HUMAN	wp04h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5655	15567	25663	3.27	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
9931	19618		4.82	7.0E-41	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
279	10244	20064	1.72	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2064	11954	21851	2.19	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4364	14260	24044	0.94	6.0E-41	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
1761	11660	21532	1.31	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79626 3'
4018	13922		0.98	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6945	15850		2.55	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
385	10332		1.91	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1082	10998	20839	1.28	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1388	11293	21149	9.42	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element ;
1388	11293	21150	9.42	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE. ;contains LTR5.b1 LTR5 repetitive element ;
1404	11309	21170	2.12	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1618	11522	21380	8.5	4.0E-41	AI500406.1	EST_HUMAN	tm96c04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2869	12787	22578	3.03	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2859	12787	22579	3.03	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4052	13954	23730	1.89	4.0E-41	X92685.1	NT	H.sapiens DNase I hypersensitive site (HSS-3) enhancer element
5920	15825		1.39	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
7590	17441	27657	6.01	4.0E-41	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
8925	18733		7.62	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAACC07 5'
9699	19510		2.31	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
932	10857	20704	1.64	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4240	14139	23914	3.08	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5047	14919		0.85	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5376	15296	25143	7.36	3.0E-41	X87689.1	NT	H.sapiens mRNA for putative p64 CLCP protein
5849	15755	25873	1.49	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
1782	11445	21305	7.3	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1915	11810	21688	2.3	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week I Homo sapiens cDNA 5' end
2172	12059	21962	1.03	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2221	12106	22010	4.07	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2798	11445	21305	5.31	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4521	14414	24199	1.06	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4521	14414	24200	1.06	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
6522	16381	26559	6.59	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
6702	16582	26772	1.33	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6702	16582	26773	1.33	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
6716	16596	26786	1.39	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week I Homo sapiens cDNA 5' end
7188	17065	27255	1.7	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
8777	18594	28882	3.46	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
4465	14359	24149	4.64	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
7420	17287	27494	1.8	1.0E-41	AI217868.1	EST_HUMAN	qf75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
9197	18930		2.63	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
6958	16836		1.33	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
7292	17168	27367	2.63	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7292	17168	27368	2.63	9.0E-42	11660151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
455	10399	20216	5.37	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2062	11952	21849	1.32	8.0E-42	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9238	19625		32.6	8.0E-42	AA493896.1	EST_HUMAN	nh07c02.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG MRNA ;
916	10840		1.83	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1812	11709	21586	3.25	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds
1812	11709	21587	3.25	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pI4K230) mRNA, complete cds

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2244	12128		3.51	6.0E-42	AW238656.1	EST_HUMAN	xp29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.t1 L1 repetitive element ;
4936	14814		1.04	6.0E-42	AI284770.1	EST_HUMAN	qu24h09.x1 NCI_CGAP_Br12 Homo sapiens cDNA clone IMAGE:1965761 similar to contains Alu repetitive element;
5355	16275	25105	1.81	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5504	15275	25105	1.72	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
131	10105		5.44	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
431	10376	20197	1.17	5.0E-42	BE217913.1	EST_HUMAN	hv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
478	10422		2.94	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
479	10423		1.27	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6016	15920	26050	1.76	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6016	15920	26051	1.76	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6072	16055	26203	2.76	5.0E-42	11417957	NT	Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
6274	16138	26294	1.57	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7098	16975	27168	2.76	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8366	18243	28494	2.15	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
736	10668	20502	8.89	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
736	10668	20503	8.89	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1050	10967	20809	2.67	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4100	14000	23779	1.61	4.0E-42	X59417.1	NT	H.sapiens PROS-27 mRNA
4156	14056	23830	4.52	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4480	14374	24162	10.26	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
8041	17932	28179	2.07	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
8041	17932	28180	2.07	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
8714	18531	28815	3.22	4.0E-42	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
98	10084		0.78	3.0E-42	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.t2 THR repetitive element ;
1467	11372	21239	3.63	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2361	12241		3.86	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2375	12255	22146	2.15	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5519	15437	25500	10.2	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGE resequences, MAGC Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5519	15437	25501	10.2	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGE resequences, MAGC Homo sapiens cDNA
7663	17513	27739	1.27	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
717	10648	20478	1.06	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1026	10944	20789	0.96	1.0E-42	AW295809.1	EST_HUMAN	UI-H-BI1-afh-e-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1085	11001	20842	1.11	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1085	11001	20843	1.11	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1222	12688	20983	12.78	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1222	12688	20984	12.78	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1673	11575	21443	1.46	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
1986	11879	21772	0.91	1.0E-42	AF110296.1	NT	Homo sapiens PDNP1 gene, exon 17
2497	12372	22264	1.98	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2935	12862	22662	8.93	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3647	13561	23347	2.15	1.0E-42	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3849	13760	23553	1.02	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4153	14053	23827	1.72	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4489	14383	24170	0.86	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4640	14528	24316	2.85	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4640	14528	24317	2.85	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PI31), mRNA
4669	14555	24348	5.35	1.0E-42	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4769	14654	24442	1.2	1.0E-42	AB033114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
5048	14920	24693	0.98	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
5048	14920	24694	0.98	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
7805	17655	27893	3.89	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
8397	18273	28525	2.84	9.0E-43	AA435719.1	EST_HUMAN	zt79a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3'
636	10573	20386	12.13	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
636	10573	20387	12.13	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
685	10618	20441	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
685	10618	20442	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
685	10618	20443	4.33	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3589	13503	23292	6.05	7.0E-43	AW246442.1	EST_HUMAN	2822251.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7092	16969		1.76	7.0E-43	AI936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7.b1 LTR7 repetitive element ;
1320	11227		10.17	6.0E-43	AA491890.1	EST_HUMAN	ne72d06.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:909803 similar to gb:L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN);
2547	12421		4.15	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADC Homo sapiens cDNA clone ADCACC10 5'
5811	15716	25829	2.02	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6128	15975	26111	2.02	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.t3 MER1 MER1 repetitive element ;
7668	17518	27746	1.83	6.0E-43	AA195154.1	EST_HUMAN	zr35e06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529641 G529641 DB1, COMPLETE CDS. ;contains element PTR7 repetitive element ;
8449	18322		6.54	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
137	10111		1.98	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
494	10437	20249	3.01	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis I Homo sapiens cDNA 5' end
2816	12745	22539	1.36	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC06 5'
7390	17308	27514	4.47	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
7945	17795	28035	2.2	5.0E-43	AI733244.1	EST_HUMAN	oo52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591 PV14 GENE. ;
7964	17814	28055	1.41	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
8145	18033	28280	5.46	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-290400-004-c02 SN0007 Homo sapiens cDNA .
8338	18215	28468	2.67	5.0E-43	W29011.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8753	17902	28146	2.6	5.0E-43	X15804.1	NT	Human mRNA for alpha-actinin
957	12643	20728	4.85	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6231	16097		1.72	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDHB6), mRNA
6757	16636	26824	4.49	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
6757	16636	26825	4.49	4.0E-43	AI244341.1	EST_HUMAN	qj76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3 MER10 repetitive element ;
8624	18489	28761	1.8	4.0E-43	T77380.1	EST_HUMAN	yd72h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'
9174	18915		1.89	4.0E-43	R20950.1	EST_HUMAN	yg06b05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
1195	11105		2.84	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1669	11571	21437	1.48	3.0E-43	X97869.1	NT	H.sapiens gene encoding La autoantigen
3524	13440	23237	1.05	3.0E-43	S69002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein {rearranged translocation} [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4193	14093	23872	0.95	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_Pr7 Homo sapiens cDNA clone IMAGE:1017419
5837	15743	25855	1.71	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
5837	15743	25856	1.71	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6037	15940	26072	3.78	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
6746	16625		6.68	3.0E-43	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.t2 THR repetitive element ;
7120	16997	27188	1.18	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
8962	18769	29061	2.02	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
177	10148		4.27	2.0E-43	AI190764.1	EST_HUMAN	qd61c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.t3 PTR7 PTR7 repetitive element ;
6312	16175	26332	1.36	2.0E-43	AW207390.1	EST_HUMAN	UI-H-BI1-afi-a-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
6836	16715		7.53	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
8532	18404		3.38	2.0E-43	T03007.1	EST_HUMAN	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3'end similar to LINE-1
1630	11534	21394	2.92	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1630	11534	21395	2.92	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1678	11580	21450	3.36	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2692	12557	22444	4.95	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
5987	15892	26014	12.07	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
5987	15892	26015	12.07	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6159	15117	24860	1.63	1.0E-43	R19751.1	EST_HUMAN	yg40e01.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38 ;
6700	16580		1.63	1.0E-43	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
7129	17006	27199	25.23	1.0E-43	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
8331	18208	28468	6.75	1.0E-43	AI984961.1	EST_HUMAN	wr87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
8672	18560	28844	3.2	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
9117	18880		3.66	1.0E-43	AL137964.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
9405	19058	25311	1.89	1.0E-43	AI675416.1	EST_HUMAN	wb99b04.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2313775 3'
9618	19196	25265	2.52	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
872	10798	20648	5.98	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
872	10798	20649	5.98	8.0E-44	AI222985.1	EST_HUMAN	qh23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
6968	16845	27037	3.87	8.0E-44	X94354.1	NT	H.sapiens DNA for Cone cGMP-PDE gene

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8504	18377	28643	3.39	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
8935	18743	29038	5.06	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
9359	19031	25304	2.59	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
9400	19369	25191	1.89	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
9742	19532	25059	1.75	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
9885	19369	25191	1.84	8.0E-44	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
643	10580		0.85	7.0E-44	R06035.1	EST_HUMAN	ye89e01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2187	12074	21978	1.2	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2937	12864	22663	2.2	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2937	12864	22664	2.2	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3786	13698	23485	2.28	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4148	14048	23821	1.17	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4148	14048	23822	1.17	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6762	16641	26828	2.05	7.0E-44	AU159839.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
8986	18791	29080	2.61	6.0E-44	AW954050.1	EST_HUMAN	EST366120 MAGE resequences, MAGC Homo sapiens cDNA
300	10264		2.52	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
329	10288		2.04	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
6605	16485	26672	3.79	5.0E-44	AI568523.1	EST_HUMAN	tn40d02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1 OFR OFR repetitive element ;
7399	17317		2.59	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3368	13287	23086	2.9	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8564	18433	28702	13.3	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1746	11646		1.07	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
2485	12360	22254	1.54	3.0E-44	BE880626.1	EST_HUMAN	601491529F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893839 5'
3059	12986	22777	5.08	3.0E-44	AA169851.1	EST_HUMAN	zp18b05.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
1033	10951	20793	2.75	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1033	10951	20794	2.75	2.0E-44	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1189	11099	20945	4.63	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1189	11099	20946	4.63	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1290	11197	21052	2.79	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1346	11252	21108	1.43	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182938 3' similar to SW:OXYB_HUMAN P22059 OXYSTEROL-BINDING PROTEIN. ;
2105	11994	21894	2.03	2.0E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2629	12403	22294	1.1	2.0E-44	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2567	12438		3.32	2.0E-44	5901933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3425	13342	23147	1.36	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4468	14362	24152	1.76	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
5709	15617	25719	1.39	2.0E-44	11449901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6097	15107	24870	1.46	2.0E-44	AF038968.1	NT	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, alternatively spliced product, complete cds
6383	16245	26406	3.86	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
6383	16245	26407	3.86	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7009	16886	27078	1.88	2.0E-44	BE389058.1	EST_HUMAN	601286914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
9022	18816		2.22	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
9710	19736	24910	2.72	2.0E-44	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
9906	19383		1.38	2.0E-44	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
46	10034	19839	3.64	1.0E-44	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
46	10034	19840	3.64	1.0E-44	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
566	10505	20312	1.85	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1179	11090		1.52	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1555	11460		5.54	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2177	12064	21965	3.53	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.t3 THR repetitive element ;
2177	12064	21966	3.53	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.t3 THR repetitive element ;
2237	12716	22024	1.05	1.0E-44	AA398099.1	EST_HUMAN	zt88g11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2732	12594	22489	1.39	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3664	13578		5.08	1.0E-44	AA455869.1	EST_HUMAN	aa01c09.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5061	14931	24702	0.81	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5061	14931	24703	0.81	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8378	18255		10.75	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
8816	18629	28918	4.18	1.0E-44	10092664	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
8869	18681	28970	3.43	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
8869	18681	28971	3.43	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4476	14370	24159	1.74	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4476	14370	24160	1.74	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2477	12353	22245	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5015	14889	24656	7.49	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
3896	13806		5.25	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
9707	19718		1.46	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
874	10800		1.11	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1957	11852	21739	5.01	5.0E-45	BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3173	13098	22904	2.01	5.0E-45	AI523766.1	EST_HUMAN	tg94f07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1. ;
5384	15303	25155	8.83	5.0E-45	AA397781.1	EST_HUMAN	zt72d03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
7226	17103	27292	1.67	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
8940	18748	29043	2.67	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1127	11041	20883	8.96	4.0E-45	X95826.1	NT	H.sapiens ART4 gene
2246	12130	22027	1.98	4.0E-45	BE265622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
9613	19192		1.62	4.0E-45	BF676077.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
3997	13210		1.17	3.0E-45	T71480.1	EST_HUMAN	yd35f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
6920	16798		1.51	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7104	16981	27173	3.44	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
7907	17757	27996	8.37	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7907	17757	27997	8.37	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9814	19660		1.33	3.0E-45	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2454	12331		2.17	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2996	12924	22716	0.93	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5929	15834	25957	4.82	2.0E-45	L01665.1	NT	*Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1*
6489	16347	26516	1.75	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8179	19471	28315	27.64	2.0E-45	BE934350.1	EST_HUMAN	MR0-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
8516	18388	28652	3.96	2.0E-45	AA458770.1	EST_HUMAN	aa87f12.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144569 G1144569 R-SLY1. ;
8794	18608	28898	2.13	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
8794	18608	28899	2.13	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
9853	19346		2.76	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
118	10349		2.22	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
403	10349		2.7	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
464	10407	20227	1.5	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1157	11070	20915	1.7	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3065	12992	22784	6.76	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3447	13364	23171	1.04	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3526	13442	23239	0.81	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4378	14274	24055	4.08	1.0E-45	BE396633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
4884	14765	24541	1.05	1.0E-45	11545796	NT	Homo sapiens niban protein (NIBAN), mRNA
7274	17151	27347	5.22	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
7485	17355	27559	1.25	1.0E-45	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
9231	18950	25358	4.3	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
9415	19067		5.38	1.0E-45	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9421	19070		2.56	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9820	19324	25207	3.17	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6790	16669	26861	2.28	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
7018	16895		6.71	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7986	17836	28077	7.89	9.0E-46	AW246984.1	EST_HUMAN	2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2392	12270	22165	8.79	8.0E-46	AI433261.1	EST_HUMAN	ti32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
2392	12270	22166	8.79	8.0E-46	AI433261.1	EST_HUMAN	ti32f08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_rna2 TUBULIN BETA-1 CHAIN (HUMAN);
6692	16572		3.97	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
4478	14372		6.54	7.0E-46	BE386165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4701	14587		1.01	7.0E-46	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
5683	15592	25693	4.01	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
5912	15818	25943	1.35	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
9543	19144		1.35	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2726	12588	22483	5.53	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element ;
2726	12588	22484	5.53	6.0E-46	AI884381.1	EST_HUMAN	wm31f08.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.t2 MER19 repetitive element ;
5727	15634	25737	8.85	6.0E-46	AI635448.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE. ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8694	17878		3.03	6.0E-46	BE784971.1	EST_HUMAN	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
197	10169		6.41	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3484	13400	23205	1.12	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3484	13400	23206	1.12	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6039	15942	26074	1.79	5.0E-46	BF590442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202 O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
6144	16017	26155	3.52	5.0E-46	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4156670 5'
625	10562		1.51	4.0E-46	AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1676	11578	21446	3.57	4.0E-46	AW770544.1	EST_HUMAN	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1676	11578	21447	3.57	4.0E-46	AW770544.1	EST_HUMAN	hl86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1 LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
2710	12573	22464	3.55	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
4320	14217	23999	1.07	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
4320	14217	24000	1.07	4.0E-46	AB014522.1	NT	Homo sapiens mRNA for KIAA0622 protein, partial cds
5338	15258	25082	1.84	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5338	15258	25083	1.84	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
9660	19221	25237	1.91	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4294	14192	23976	0.8	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA
4666	14552	24343	1.13	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4666	14552	24344	1.13	3.0E-46	Z73660.1	NT	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
7081	16958	27151	8.3	3.0E-46	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
8856	18668	28955	2.63	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
819	10747	20594	5.91	2.0E-46	AA468646.1	EST_HUMAN	ne08a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1542	11447		1.32	2.0E-46	AA678246.1	EST_HUMAN	zi27a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1623	11527	21385	2.43	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4899	14779	24555	1.15	2.0E-46	AA399286.1	EST_HUMAN	zt59e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN. ;
6418	16280	26442	6.78	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
6703	16583		1.17	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
8571	18439		1.87	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
9157	19629		1.75	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
9409	19525		1.44	2.0E-46	H48391.1	EST_HUMAN	yr32d01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:206977 5'
9728	19515	25136	3.81	2.0E-46	AW277214.1	EST_HUMAN	xq78h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1213	11121	20970	5.19	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2236	12121	22023	4.6	1.0E-46	AW978516.1	EST_HUMAN	EST390625 MAGE resequences, MAGP Homo sapiens cDNA
2351	12231	22128	2.59	1.0E-46	H97330.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3211	13135	22936	2.81	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H.sapiens MT-1l mRNA. (HUMAN);
4772	14656		2.64	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5495	15414	25477	4.18	1.0E-46	BF194707.1	EST_HUMAN	7o92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5636	19449	25639	5.66	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
5636	19449	25640	5.66	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
8236	15414	25477	4.26	1.0E-46	BF194707.1	EST_HUMAN	7o92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
9188	18923	25348	1.43	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
9188	18923	25349	1.43	1.0E-46	BF531102.1	EST_HUMAN	602072264F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215398 5'
9925	19397		1.53	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
749	10679		4.51	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
4848	14729	24512	2.61	9.0E-47	AW770928.1	EST_HUMAN	hl93e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703 HYPOTHETICAL 12.4 KD PROTEIN. ;
9682	19617	25001	1.84	9.0E-47	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1766	11665	21539	14.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
1766	11665	21540	14.02	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2684	12549	22439	1.74	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2989	12917	22712	1.72	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
2501	12376	22266	3.05	6.0E-47	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7344	17212	27411	6.27	6.0E-47	AI695189.1	EST_HUMAN	tz98h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296659 3'
5963	15868	25990	5.27	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
8174	18062		3.91	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCF07

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1379	11284	21140	3.41	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6938	16816	27008	2.06	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
6938	16816	27009	2.06	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8905	18713		4.84	4.0E-47	AW515509.1	EST_HUMAN	xx66b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1] ;
532	10474	20287	1.75	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
532	10474	20288	1.75	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
801	10730	20571	5.17	3.0E-47	N57483.1	EST_HUMAN	yy54b04.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277327 3'
930	10855	20703	8.9	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1984	11877	21770	1.5	3.0E-47	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
3885	13796		4.99	3.0E-47	U93181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4265	14164	23941	0.97	3.0E-47	M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5659	15571	25666	4.26	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
5659	15571	25667	4.26	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adx-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
5953	15858		1.89	3.0E-47	AI222413.1	EST_HUMAN	qh04e07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
142	10116	19936	4.27	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
952	10876	20722	2.18	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
952	10876	20723	2.18	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1548	11453		1.18	2.0E-47	AI969279.1	EST_HUMAN	wq96b02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2479851 3'
1575	11479	21338	1.22	2.0E-47	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1654	11557	21420	4.44	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
2185	12072	21974	2.3	2.0E-47	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
4251	14150	23924	1.66	2.0E-47	4504866	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4287	14186	23967	1.75	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4287	14186	23968	1.75	2.0E-47	AA569592.1	EST_HUMAN	nf23g07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:914652
4406	14300	24084	2.06	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
4707	14593	24384	1.1	2.0E-47	AW965166.1	EST_HUMAN	EST377239 MAGE resequences, MAGI Homo sapiens cDNA
5635	15549	25637	1.6	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
5635	15549	25638	1.6	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6532	19464		1.33	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
6643	16523	26716	2.1	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6643	16523	26717	2.1	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7060	16937	27127	1.77	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9070	10116	19936	5.77	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9219	19658	24988	1.98	2.0E-47	R42423.1	EST_HUMAN	yf92e08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:28966 3' similar to contains OFR repetitive element ;
9257	19659		1.32	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1383	11288	21142	4.5	1.0E-47	AI333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3749	13662	23443	0.79	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3749	13662	23444	0.79	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5008	14882	24648	2.59	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-h02 ST0197 Homo sapiens cDNA
6194	15954	26086	7.68	1.0E-47	AI880886.1	EST_HUMAN	at19e06.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN);
7928	17778	28017	1.76	1.0E-47	L30115.1	NT	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
1595	11499	21358	2.34	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3509	13425	23228	0.83	9.0E-48	BF359947.1	EST_HUMAN	CM2-MT0100-310700-290-f05 MT0100 Homo sapiens cDNA
8460	18333	28595	3.22	9.0E-48	BE393813.1	EST_HUMAN	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1230	11138		1.32	8.0E-48	4501900	NT	Homo sapiens aminoacylase 1 (ACY1), mRNA
1231	11138		1.51	8.0E-48	4501900	NT	Homo sapiens aminoacylase 1 (ACY1), mRNA
3096	13023	22818	3.62	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3096	13023	22819	3.62	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
482	10426		1.37	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
483	10426		13.37	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1482	11387	21250	1.12	7.0E-48	6912719	NT	Homo sapiens tousled-like kinase 1 (TLK1), mRNA
1620	11524	21382	3.49	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
5947	15852	25975	22.88	7.0E-48	11416831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
7276	17152	27348	1.52	6.0E-48	AF026816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
7500	17370	27577	1.9	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
7587	17438	27654	3.38	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
3269	15067	22989	1.39	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
8325	18202	28451	3.55	4.0E-48	AI620420.1	EST_HUMAN	tu47a02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2254154 3'
1363	11269	21124	0.92	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
1933	11828	21710	18.97	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1933	11828	21711	18.97	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

Table 4

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3579	13493	23284	0.88	3.0E-48	AW664531.1	EST_HUMAN	hi14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
5592	15507	25582	2.35	3.0E-48	BE084571.1	EST_HUMAN	MR4-BT0657-060400-201-e10 BT0657 Homo sapiens cDNA
6889	16768		2.86	3.0E-48	AA659930.1	EST_HUMAN	nv03f05.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element ;
8248	18128	28376	7.08	3.0E-48	BF514170.1	EST_HUMAN	UI-H-BW1-ani-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
39	10027	19827	1.18	2.0E-48	AA631940.1	EST_HUMAN	fmfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4431	14326	24114	1.35	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5553	15469	25539	72.29	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
5553	15469	25540	72.29	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1101072 3'
6440	16301	26464	4.29	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6440	16301	26465	4.29	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6447	16308	26473	2.9	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
6864	16743	26936	2.39	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
9184	15082	24828	2.45	2.0E-48	AA465007.1	EST_HUMAN	zx80c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
9511	19579	25070	1.63	2.0E-48	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
50	10037	19844	0.85	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
855	10782	20632	6.93	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1274	11182	21032	3.26	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1876	11772	21648	44.65	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3443	13360	23167	1.23	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5082	14952	24728	1.1	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6303	16167	26325	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
7337	17205	27404	5.72	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
7526	17377	27586	4.48	1.0E-48	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
7934	17784	28023	5.06	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
7934	17784	28024	5.06	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
8999	18802	29094	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8999	18802	29095	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
9145	19606		1.56	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
5692	15601	25702	2.95	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5692	15601	25703	2.95	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6827	16706	26900	3.19	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
134	10335	20157	1.47	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
134	10335	20158	1.47	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	10335	20157	1.74	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
388	10335	20158	1.74	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	10335	20157	1.99	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	10335	20158	1.99	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1202	11112	20958	4.05	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4560	14443	24227	0.95	7.0E-49	O60811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.3
5351	15271	25100	1.93	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923 O54923 RSEC15. ;
5357	15277	25107	1.34	7.0E-49	AL120937.1	EST_HUMAN	DKFZp762C033_s1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
190	10162	19979	11.77	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
8600	18467	28738	2.92	6.0E-49	AW452218.1	EST_HUMAN	UI-H-BI3-alo-a-05-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
8920	18728	29022	2.69	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8920	18728	29023	2.69	6.0E-49	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
9507	19498		3.43	6.0E-49	AA707567.1	EST_HUMAN	zj29c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
695	10628	20452	3.37	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
695	10628	20453	3.37	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1753	11653	21524	1.94	5.0E-49	AA172121.1	EST_HUMAN	zp29c07.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 LTR7 repetitive element ;
2721	12583	22477	5.18	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3235	13159	22957	5.13	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1) (H. sapiens) (LOC63362), mRNA
514	10456	20266	37.46	4.0E-49	AW189533.1	EST_HUMAN	xl08b01.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703 ;
9376	19710		2.43	4.0E-49	AA210798.1	EST_HUMAN	zr90f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'
9459	19090		3.3	4.0E-49	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
548	10489	20298	0.93	3.0E-49	X68968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2611	12479		2.01	3.0E-49	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element ;
4909	14788	24564	2.08	3.0E-49	U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40
6386	16248	26409	9.6	3.0E-49	H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12
8621	18487	28759	2.3	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
645	10582		2.66	2.0E-49	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
3185	13110	22914	1.4	2.0E-49	N26446.1	EST_HUMAN	yx23d06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262571 5'
3521	13437	23235	0.93	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
4693	14579	24373	1.12	2.0E-49	AI167357.1	EST_HUMAN	oz88d02.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);contains Alu repetitive element;contains element MER22 repetitive element ;
4704	14590	24381	1.25	2.0E-49	BF511846.1	EST_HUMAN	UI-H-BI4-aps-d-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
6040	15943	26075	1.47	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
6717	16597		1.97	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCY50
9467	19599		1.53	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
881	10807		3.95	1.0E-49	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1760	11659	21531	2.58	1.0E-49	BE255216.1	EST_HUMAN	601115769F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5289	15210	25011	4.97	1.0E-49	BF131007.1	EST_HUMAN	601820053F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6287	16151	26307	2.93	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6287	16151	26308	2.93	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
6322	16185	26346	2.17	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6322	16185	26347	2.17	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6709	16589	26777	1.29	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
6709	16589	26778	1.29	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7200	17077	27262	1.22	1.0E-49	BE409340.1	EST_HUMAN	601300992F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
7830	17680	27924	1.21	1.0E-49	AL043129.2	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
8630	18495	28769	3.88	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
9018	18813		1.73	1.0E-49	BE159343.1	EST_HUMAN	MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA
9367	19035		2	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
4923	14802		1.06	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
163	10136	19951	2.59	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
702	10635	20460	1.89	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
702	10635	20461	1.89	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1016	10934		1.21	8.0E-50	AF000573.1	NT	Homo sapiens homogentisate 1,2-dioxygenase gene, complete cds
1727	11628	21497	2.51	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2432	12309	22204	1.36	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2432	12309	22205	1.36	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2666	12531	22421	1.69	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
8711	18528	28811	2.1	8.0E-50	AA633467.1	EST_HUMAN	np62d06.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459 GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN);
603	10539	20349	0.96	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
8139	18027	28273	9.52	7.0E-50	AI872137.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'
6781	16660		4.47	6.0E-50	BE044076.1	EST_HUMAN	ho36h04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
8190	18076	28326	3.17	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
8190	18076	28327	3.17	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1752	11652	21522	0.85	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1752	11652	21523	0.85	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
7255	17132		5.64	5.0E-50	AA557683.1	EST_HUMAN	nl45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element ;
8991	18795	29086	1.85	5.0E-50	AA403053.1	EST_HUMAN	zt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769 G1335769 GAG-POL POLYPROTEIN. ;
899	10824		1.29	4.0E-50	AA601143.1	EST_HUMAN	no54e09.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1896	11791		2.45	3.0E-50	M18048.1	NT	Human endogenous retrovirus RTVL-H2
3259	13182	22981	1.14	3.0E-50	AA746142.1	EST_HUMAN	ob03f06.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
3692	13606	23392	4.6	3.0E-50	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
6056	16039	26180	1.55	3.0E-50	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
6505	16364	26540	4.01	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
6505	16364	26541	4.01	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7649	17499	27721	1.17	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
8760	17909	28153	5.94	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
761	10691		4.91	2.0E-50	AF055066.1	NT	Homo sapiens MHC class 1 region
1063	10979	20823	4.6	2.0E-50	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
1425	11330	21197	18.02	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
6924	16802	26995	6.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
6924	16802	26996	6.27	2.0E-50	X06956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
7686	17536	27761	1.53	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
7686	17536	27762	1.53	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
235	10204	20018	1	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
235	10204	20019	1	1.0E-50	BE007080.1	EST_HUMAN	PM3-BN0137-290300-002-g11 BN0137 Homo sapiens cDNA
454	10398	20215	2.1	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2314	12195		8.98	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
7375	17244	27450	1.22	9.0E-51	AA043738.1	EST_HUMAN	zk51c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
4467	14361	24151	4.89	8.0E-51	AA610842.1	EST_HUMAN	np98e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6510	16369	26546	2.34	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7448	17257		1.28	8.0E-51	AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3245	13168	22967	1.36	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3317	13238	23042	0.83	7.0E-51	AW274720.1	EST_HUMAN	xn34a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;
4076	13978	23757	1.26	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4076	13978	23758	1.26	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4254	14153	23927	2.38	7.0E-51	AW295603.1	EST_HUMAN	UI-H-BW0-aip-b-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1936	11831	21714	5.3	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3428	13345	23150	12.92	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4212	14110	23887	0.78	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4212	14110	23888	0.78	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5646	15558	25651	2.26	6.0E-51	X01788.1	NT	Human haptoglobin related (Hpr) gene exon 3
5650	15562	25656	6.68	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
5650	15562	25657	6.68	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6158	15116	24859	2.16	6.0E-51	11429665	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
7583	17434	27649	2.26	6.0E-51	7661535	NT	Homo sapiens B9 protein (B9), mRNA
8580	18448	28716	1.72	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
774	10704	20543	10.92	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
786	10715	20557	1.47	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
975	12682	20745	1.37	5.0E-51	AL133204.1	NT	Novel human gene mapping to chomosome X
1590	11494	21354	0.84	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2548	12422	22311	11.48	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3863	13774	23566	1.08	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3863	13774	23567	1.08	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5004	14879	24643	2.34	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8601	18468	28739	3.72	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
130	10104	19926	0.92	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1159	11072	20917	4.16	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4232	14130	23906	2.13	3.0E-51	AL169142.1	NT	Novel human gene mapping to chomosome 22
6474	16333	26500	1.73	3.0E-51	R15914.1	EST_HUMAN	ya47c08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);contains LTR5 repetitive element ;
7131	17008		5.87	3.0E-51	M29063.1	NT	Human hnRNP C2 protein mRNA
9675	19233		1.58	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
362	10318	20139	1.81	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
673	10607	20424	1.08	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
673	10607	20425	1.08	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1662	11564	21431	2.24	2.0E-51	AA233352.1	EST_HUMAN	zr30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTVL-H PROTEIN. ;contains LTR7.t3 LTR7 repetitive element ;
3672	13586	23373	2.21	2.0E-51	AI492415.1	EST_HUMAN	ti27g03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4392	14288	24071	1.02	2.0E-51	AW137826.1	EST_HUMAN	UI-H-BI1-adj-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5662	15573	25670	2.96	2.0E-51	BE782015.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7047	16924	27114	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
7047	16924	27115	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
7478	17348	27552	1.68	2.0E-51	AI917078.1	EST_HUMAN	ts74a07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
7539	17390	27600	5.25	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7962	17812	28054	1.71	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
8640	15259	25084	8.63	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
8640	15259	25085	8.63	2.0E-51	AI732851.1	EST_HUMAN	ob34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
9668	19227	25240	1.33	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
109	10090	19905	4.4	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1478	11383		22.7	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
4309	14206	23989	0.96	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4309	14206	23990	0.96	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5310	15231	25036	3.12	1.0E-51	T18862.1	EST_HUMAN	b12056t Testis 1 Homo sapiens cDNA clone b12056
8989	19771		3.57	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSCBB02 5'
9454	19086		3.28	9.0E-52	AA777621.1	EST_HUMAN	zi95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448600 3' similar to contains THR.t3 THR repetitive element ;
146	10120	19939	7.31	8.0E-52	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.t3 THR repetitive element ;
1481	11386	21249	1.33	8.0E-52	X84900.1	NT	H.sapiens mRNA for laminin-5, alpha3b chain
1633	11537	21397	2.05	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1633	11537	21398	2.05	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3913	11537	21397	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3913	11537	21398	6.44	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7211	17088	27278	1.48	7.0E-52	W56471.1	EST_HUMAN	zc59a06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element;
1170	11082		0.86	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271299-049-d07 BT0537 Homo sapiens cDNA
1668	11570	21436	2.25	6.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
8540	18412	28678	2.23	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4340	14237	24021	2.07	5.0E-52	Z78898.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
1639	11543	21402	0.93	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1748	11648	21516	8.58	4.0E-52	4758843	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
3850	13761	23554	0.82	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
6686	16566	26760	1.24	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915836 5'
6965	16843	27035	7.25	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
9291	18992		4.25	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9778	19293		5.09	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4002	13908		9.98	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
550	10491	20299	1.39	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
550	10491	20300	1.39	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2450	12327	22226	1.75	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2706	12569		20.53	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4902	14782	24557	2.74	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5497	15416	25479	2.74	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231299-053-E12 CT0214 Homo sapiens cDNA
5841	15747	25860	1.49	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
7028	16905		8.39	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
7458	17267		1.98	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
7825	17675	27918	4.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7826	17675	27919	4.53	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8536	18408	28671	5.33	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
8536	18408	28672	5.33	2.0E-52	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
8547	18419	28689	3.09	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
8659	18548		2.08	2.0E-52	W70260.1	EST_HUMAN	zd49g12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
8891	18701		3.22	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
9101	19755	24894	8.86	2.0E-52	AW236297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element;contains element LTR2 repetitive element ;
9496	19112		4.28	2.0E-52	AI808985.1	EST_HUMAN	wf67d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859 Q16859 CARBOXYLESTERASE ;
522	10464	20276	1.37	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1349	11255	21111	8.25	1.0E-52	4504026	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
2489	12364		1.2	1.0E-52	4502238	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
3021	12949	22741	1.41	1.0E-52	S61070.1	NT	pol=reverse transcriptase homolog {retroviral element} [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
5270	15192	24967	3.59	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5851	15757	25875	2.11	1.0E-52	U38964.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
6394	16256	26417	3.19	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
6932	16810		1.64	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8023	17873		1.61	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8147	18035	28283	1.84	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
8210	18094		2.04	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
3723	13635	23420	1.03	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4293	14191	23975	1.01	9.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
4966	14841	24611	0.93	9.0E-53	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
9338	19018		2.06	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
9752	19632		2.98	7.0E-53	AI421782.1	EST_HUMAN	tf44f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2099077 3' similar to contains THR.t1 THR repetitive element ;
4009	13915	23690	2.2	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
9389	19048		1.72	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
43	10031	19834	1.92	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
43	10031	19835	1.92	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4715	14601	24387	1.09	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
8545	18417	28685	3.33	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
8545	18417	28686	3.33	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2625	12493	22384	2.59	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3670	13584	23371	1.29	3.0E-53	AW050836.1	EST_HUMAN	wz22c07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4486	14380	24167	1.18	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
4833	14715	24498	0.85	3.0E-53	BE069344.1	EST_HUMAN	QV3-BT0381-270100-073-d06 BT0381 Homo sapiens cDNA
6833	16712	26905	9.88	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
7238	17115		8.59	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
450	10394		4.25	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2279	12163	22060	2.98	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID. NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2490	12365		10.54	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
2694	12559	22446	6.93	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2694	12559	22447	6.93	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3207	13131	22933	1.18	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
3970	13877	23653	2.06	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
4390	14286	24068	1.07	2.0E-53	4506962	NT	Homo sapiens SKAP55 homologue (SKAP-HOM) mRNA
5091	14961	24735	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5091	14961	24736	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5331	15251	25056	3.11	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5331	15251	25057	3.11	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
7413	17280		5.6	2.0E-53	AW245676.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1429	11334	21200	0.9	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudoautosomal region; segment 2/2
3364	13283	23083	1	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6021	15925	26056	1.42	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7252	17129	27322	5.14	1.0E-53	X79536.1	NT	H.sapiens mRNA for hnRNPcore protein A1
5152	15019	24787	0.8	9.0E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5152	15019	24788	0.8	9.0E-54	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5244	19439	24939	4.71	9.0E-54	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
200	10172	19988	3.09	8.0E-54	BE386785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1794	11692	21568	1.33	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4629	14517	24307	1.25	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4629	14517	24308	1.25	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	14517	24307	1.08	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5030	14517	24308	1.08	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
5614	15529	25612	20.81	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
379	10363	20186	1.26	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.t3 MER30 repetitive element ;
1789	11687	21563	1.54	7.0E-54	Y16645.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2158	12045	21945	4.61	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element ;

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7831	17681	27925	2.23	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
8611	18478		6.24	7.0E-54	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
22	10009	19802	1.64	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
1833	11730	21605	0.87	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1833	11730	21606	0.87	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3246	13169	22968	0.84	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3923	13832	23612	2.4	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4359	14255	24040	1.24	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4774	14658		1.71	6.0E-54	Y09846.1	NT	H.sapiens shc pseudogene, p66 isoform
4930	14658		1.3	6.0E-54	Y09846.1	NT	H.sapiens shc pseudogene, p66 isoform
8750	17899	28143	1.77	6.0E-54	AW813567.1	EST_HUMAN	RC3-ST0197-151099-011-f08 ST0197 Homo sapiens cDNA
2104	11993	21893	2.25	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
176	10147		106.86	4.0E-54	AF110103.1	NT	Tupaia belangeri beta-actin mRNA, partial cds
940	10865	20712	41.94	4.0E-54	AA306764.1	EST_HUMAN	EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1764	11663	21536	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1764	11663	21537	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3168	13093		1.17	4.0E-54	AI935086.1	EST_HUMAN	wd26d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
88	10072	19888	5.11	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2522	12396	22287	0.92	3.0E-54	AL110383.1	EST_HUMAN	DKFZp434E0731_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0731 5'
2583	12454		0.88	3.0E-54	AI908757.1	EST_HUMAN	IL-BT189-190399-007 BT189 Homo sapiens cDNA
5598	16512	25590	1.48	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
6373	16235	26394	1.68	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
6373	16235	26395	1.68	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
8435	18309	28565	4.17	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
8675	18563	28847	3.34	3.0E-54	AA393362.1	EST_HUMAN	zt70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
9199	18932	25353	2.86	3.0E-54	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGC Homo sapiens cDNA
9242	19714		7	3.0E-54	AW748965.1	EST_HUMAN	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
626	10563	20374	6.29	2.0E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1342	11248	21105	1.94	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1529	11434	21290	1.6	2.0E-54	AA655008.1	EST_HUMAN	nt78a09.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element ;
2493	12367	22261	1.3	2.0E-54	AW163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:CUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2556	12428	22321	1.82	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010 .
2865	12793	22587	1.65	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3501	13418		4.06	2.0E-54	AA532925.1	EST_HUMAN	nj45g09.s1 NCI_CGAP_Pr9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
4110	14010		2.03	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4343	14240		1.13	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4780	14664	24450	1.45	2.0E-54	7706446	NT	Homo sapiens peptidylarginine deiminase type III (LOC51702), mRNA
5156	15023	24790	0.84	2.0E-54	AF083823.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 7
5363	15283	25116	3.75	2.0E-54	4759069	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5440	15360	25417	1.34	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5521	15439	25503	3.59	2.0E-54	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5673	15488	25564	18.19	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5573	15488	25565	18.19	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6227	16093	26243	8.14	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
7552	17403	27617	3.62	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7749	17599	27821	1.26	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
8963	18770		2.57	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
9693	19244	25216	1.46	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4363	14259		1.07	1.0E-54	BF315418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
9852	19345		2.26	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zrv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
1294	11201		14.56	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1297	11204		2.32	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
8530	18402		2.76	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
1065	10981	20826	1.19	7.0E-55	R09346.1	EST_HUMAN	yf26e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP:C561_BOVIN P10897 CYTOCHROME ;
7297	17173	27373	1.26	7.0E-55	AA889581.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
7315	17191	27393	1.59	7.0E-55	AU139909.1	EST_HUMAN	AU139909 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8541	18413	28679	12.75	7.0E-55	AI561056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
8541	18413	28680	12.75	7.0E-55	AI561056.1	EST_HUMAN	tq29f09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
9823	19648		4.3	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
8803	18617	28908	1.98	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1732	11633	21500	1.12	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1732	11633	21501	1.12	5.0E-55	AA704971.1	EST_HUMAN	zj95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
5941	15846	25969	1.82	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
5941	15846	25970	1.82	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7229	17106	27296	2.06	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
7770	17620	27851	1.86	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
7770	17620	27852	1.86	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
7869	17719	27965	1.19	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
9283	18985		2.13	5.0E-55	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
49	12658	19843	1.36	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
656	10591	20409	33.95	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1422	11328	21193	1.89	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1422	11328	21194	1.89	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1498	11402		1.26	4.0E-55	BF061411.1	EST_HUMAN	7j52b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.t3 L1 repetitive element ;
1979	11872	21763	1.53	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
1979	11872	21764	1.53	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2039	11930	21824	7.73	4.0E-55	4503314	NT	*Homo sapiens diacylglycerol kinase, gamma* (90kD) (DGKG) *mRNA*
2039	11930	21825	7.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2262	12146	22046	1.25	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
2545	12419		1.04	4.0E-55	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
3242	13165	22964	1.38	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6857	16736		6.44	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8559	18429		4.46	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
9200	18933		2.38	4.0E-55	BF303941.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
9138	18894		2.76	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
9866	19356		1.65	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
373	10327	20160	2.3	2.0E-55	X67147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
639	10480		0.89	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
633	10570	20383	3.08	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2928	12855	22656	0.79	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4665	14551	24342	2.97	2.0E-55	BE719986.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7284	17160		4.3	2.0E-55	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element ;
8319	18196	28446	2.2	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
91	10075	19891	1.6	1.0E-55	4505060	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
182	10154	19969	11.9	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1132	11046	20888	3.55	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1907	11802	21680	0.86	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1907	11802	21681	0.86	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2277	12161		2.3	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2290	12651	22071	1.03	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2470	12346	22238	33.19	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2507	12381	22271	4.71	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2507	12381	22272	4.71	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2568	12439	22331	1.35	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3363	13282	23082	1.16	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
3907	13817	23597	3.47	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4197	14097	23878	1.04	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4721	14607	24392	0.98	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4721	14607	24393	0.98	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5081	14951	24727	1.19	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5794	15700	25809	5.75	1.0E-55	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
5794	15700	25810	5.75	1.0E-55	11433046	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8284	18163	28405	4.74	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8284	18163	28406	4.74	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8745	17894	28138	2.58	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
8859	18671	28959	2.04	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
6358	16221	26383	1.81	9.0E-56	BE379074.1	EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
2703	12567	22457	5.18	7.0E-56	H19934.1	EST_HUMAN	yn62g03.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element ;
6504	16363	26538	1.84	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6504	16363	26539	1.84	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1666	11568	21434	2.26	5.0E-56	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
7940	17790		1.31	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
9376	19701	24902	2.68	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
25	10012	19805	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
25	10012	19806	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2676	12541	22431	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2676	12541	22432	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2781	10457	20268	3.05	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5788	15694	25802	6.29	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
5788	15694	25803	6.29	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
7999	17849	28090	1.23	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
8295	18174	28417	8.75	4.0E-56	AI498066.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
8295	18174	28418	8.75	4.0E-56	AI498066.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163046 3'
1318	11225	21081	9.85	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
2103	11992	21892	2.7	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3086	13013	22804	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3086	13013	22805	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3761	13674		1.39	3.0E-56	AF055066.1	NT	Homo sapiens MHC class 1 region
4327	14224	24006	4.05	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4470	14364	24154	2.14	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5486	15405	25467	1.57	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5486	15405	25468	1.57	3.0E-56	4759163	NT	Homo sapiens sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6109	16003	26141	6.34	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7117	16994	27185	5.74	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
7987	17837	28078	1.52	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
8124	18012	28259	10.72	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
8632	18497	28771	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
8632	18497	28772	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
9240	18955	25315	2.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
9240	18955	25316	2.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
513	10455		2.94	2.0E-56	AA199818.1	EST_HUMAN	zq52a08.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645206 3'
716	12675	20476	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
716	12675	20477	1.19	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2334	12215	22113	1.02	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2334	12215	22114	1.02	2.0E-56	M26061.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2959	12886	22684	0.93	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3489	13405	23210	1.08	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
964	10887		1.44	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3622	13536	23321	1.79	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
3622	13536	23322	1.79	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
4963	14838	24606	1.52	1.0E-56	AI905162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
7780	17630	27863	1.86	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
609	10545		1.97	9.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
4109	14009	23786	1.17	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4109	14009	23787	1.17	9.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
13	9999	19790	1.55	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
294	10258	20079	2.91	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
866	10792	20642	5.79	8.0E-57	AW264599.1	EST_HUMAN	xr05d10.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
1774	11673	21651	1.63	8.0E-57	AA496109.1	EST_HUMAN	zv51b12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
3335	13255	23060	1.02	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
3335	13255	23061	1.02	8.0E-57	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
5107	14975	24750	0.96	8.0E-57	AA971001.1	EST_HUMAN	op67h02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1581939 3'
5207	19624	25004	6.35	8.0E-57	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5888	15794	25915	11.76	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
5888	15794	25916	11.76	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6557	16416	26594	67.76	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6557	16415	26595	67.76	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8771	9999	19790	3.32	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
9468	19097		1.27	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA
9607	19188	25251	2.02	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9622	19188	25251	1.39	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2592	12462	22353	2.02	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2592	12462	22354	2.02	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3212	13136	22937	0.92	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3212	13136	22938	0.92	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3233	13157	22956	6.49	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3801	13713	23500	2.17	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
3801	13713	23501	2.17	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9934	19656		2.99	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
3694	13608	23393	1.23	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4935	14813	24581	0.96	4.0E-57	BE783649.1	EST_HUMAN	601471226F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874135 5'
787	10716	20558	0.79	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1309	11215		11.34	3.0E-57	AA230279.1	EST_HUMAN	nc13f07.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN P46783 40S RIBOSOMAL PROTEIN S10. ;
2342	12222	22119	2.83	3.0E-57	AA348335.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
2670	12535	22425	1.62	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;
2670	12535	22426	1.62	3.0E-57	BE676622.1	EST_HUMAN	7f33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2 CE20263 ;
3514	13430	23230	1.15	3.0E-57	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cln) gene, complete cds
3639	13553		115.94	3.0E-57	AW853964.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
5723	15630	25733	3.34	3.0E-57	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6736	16615	26805	3.95	3.0E-57	W28130.1	EST_HUMAN	42f6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6751	16630	26817	1.95	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
6751	16630	26818	1.95	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
7142	17019	27212	4.65	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
8279	18159	28400	20.31	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
9247	19721	24907	5.2	3.0E-57	W23871.1	EST_HUMAN	zb45d11.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
9608	19628		2.15	3.0E-57	AW178575.1	EST_HUMAN	RC0-HT0112-080999-001-C06 HT0112 Homo sapiens cDNA
2699	12563	22453	1.19	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
3392	13309		2.91	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3504	13421	23223	0.84	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3504	13421	23224	0.84	2.0E-57	R07702.1	EST_HUMAN	ye98h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4409	14303	24086	6.88	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5478	15398		1.43	2.0E-57	AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element ;
5676	15585		28.14	2.0E-57	BF115266.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.t1 MER22 repetitive element ;
7017	16894	27084	1.29	2.0E-57	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
7665	17515	27742	1.71	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
8592	18460	28729	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
8592	18460	28730	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
2184	12071	21973	1.12	1.0E-57	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
7045	16922		2.08	1.0E-57	BE043031.1	EST_HUMAN	ho32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN ;
9401	19055		3.47	1.0E-57	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element ;
9663	19223	25238	1.43	9.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
574	10512		1.41	8.0E-58	BE868715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
638	10575	20389	2.62	8.0E-58	AI798376.1	EST_HUMAN	tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
638	10575	20390	2.62	8.0E-58	AI798376.1	EST_HUMAN	tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1813	11710	21688	2.23	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1813	11710	21689	2.23	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2945	12872		2.83	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
8231	18112		5.61	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
8300	18179	28425	3.25	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BN0-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
8300	18179	28426	3.25	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BN0-ali-g-10-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2207	12094	21997	0.9	6.0E-58	BE395061.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2324	12205	22105	2.96	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2871	12798	22592	1.19	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2871	12798	22593	1.19	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
7909	17759	28000	1.3	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
9492	19109		1.8	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value.	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
297	10261	20081	2.9	5.0E-58	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
693	10626	20461	5.87	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1176	11088	20932	4.47	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1176	11088	20933	4.47	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	11088	20932	2.99	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1177	11088	20933	2.99	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3281	13202	23002	3.56	5.0E-58	AA988183.1	EST_HUMAN	or98e07.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
5458	15378		2.21	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
5748	15656	25764	5.86	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'
5894	15800	25924	1.45	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
6647	16527	26721	6.77	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
7829	17679	27923	1.56	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
9215	19650		3.26	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
9876	19362		2.49	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
369	10325	20147	17.97	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
779	10709	20548	1.58	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1452	11357	21221	1.24	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2531	12405	22297	0.97	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2590	12461	22351	2.7	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3283	13204	23004	1.1	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3680	13594	23380	2.11	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
8651	18515	28798	7.54	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
332	10291		1.17	3.0E-58	R17879.1	EST_HUMAN	yg10e02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31693 5'
1367	11273	21129	2.34	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3141	13066	22864	2.91	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3141	13066	22865	2.91	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6002	15907	26031	1.39	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DCAAZG04 5'
925	10850	20698	8.16	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
1268	11175		12.06	2.0E-58	BE208532.1	EST_HUMAN	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5288	19441	24986	4.42	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5288	19441	25010	4.42	2.0E-58	BE907186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5721	15628	25731	1.74	2.0E-58	AI124874.1	EST_HUMAN	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME\; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6246	16112	26263	2.76	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6246	16112	26264	2.76	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
8123	18011	28258	10.79	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
8332	18209	28459	2.26	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
705	10638	20463	0.93	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3'end
1052	10969	20811	5.45	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1305	11212	21067	2.17	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1305	11212	21068	2.17	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1375	11281	21136	1.07	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1641	11545	21406	2.02	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196935 3'
2771	12633	22527	0.96	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA
3493	13409	23215	0.98	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3493	13409	23216	0.98	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3659	13573	23360	0.84	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
4627	14515	24306	0.89	1.0E-58	M95963.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 4
4895	14775	24553	4.86	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
7146	17023	27217	6.7	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8985	18790		3.46	1.0E-58	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2182	12069	21971	27.47	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6759	16638	26826	1.2	8.0E-59	AI761963.1	EST_HUMAN	wh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
171	12660		1.63	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3088	13016	22807	6.21	5.0E-59	AI807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4559	14451	24237	5.85	5.0E-59	X83497.1	NT	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
6173	15130	24850	7.46	5.0E-59	AW162304.1	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element ;
7596	17447	27662	1.71	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
8278	18168	28399	2.8	5.0E-59	11434908	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
776	10706	20546	2.42	4.0E-59	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
4685	14571	24368	1.2	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4685	14671	24369	1.2	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
9366	19586		2.16	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
9	9995		5.96	3.0E-59	AW965524.1	EST_HUMAN	EST377582 MAGE resequences, MAGI Homo sapiens cDNA
221	10191	20002	4.12	3.0E-59	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1682	11584	21455	9.87	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1682	11584	21456	9.87	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2082	11972	21866	7.68	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2082	11972	21867	7.68	3.0E-59	AB029035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3090	13017	22811	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3090	13017	22812	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3753	13666	23449	1.17	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4683	14569	24366	1.07	3.0E-59	4759329	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY) mRNA
4734	14619	24406	1.85	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
5772	15679	25786	2.03	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
6352	16215	26377	1.82	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
6629	16509	26697	1.23	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
6629	16509	26698	1.23	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
9333	19014		1.64	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9474	19101		3.9	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
7555	17406		5.01	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
8003	17853		2.47	2.0E-59	BF365554.1	EST_HUMAN	RC0-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA
8205	18089	28341	1.84	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
8205	18089	28342	1.84	2.0E-59	AW410698.1	EST_HUMAN	fh07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961654 5'
9235	18953	25359	5.14	2.0E-59	AI631809.1	EST_HUMAN	wa36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542 Q86542 RTVL-H PROTEIN. ;contains LTR7.b1 LTR7 repetitive element ;
9756	19611	24997	2.75	2.0E-59	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
157	10131		3.58	1.0E-59	BE296411.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2575	12446		2.46	1.0E-59	AA748468.1	EST_HUMAN	oa56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
6463	16322	26488	1.29	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
7400	17318	27524	1.22	1.0E-59	11419630	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
8229	16322	26488	8.32	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
1455	11360	21224	2.71	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2125	12013	21911	2.7	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2125	12013	21912	2.7	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
5640	15553	25645	1.41	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6644	16524	26718	2.6	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
7174	17051	27240	2.26	8.0E-60	11428949	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
7451	17260	27465	1.68	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7451	17260	27466	1.68	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8207	18091	28344	5.38	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8207	18091	28345	5.38	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
737	10669	20504	6.69	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
738	10669	20504	32.94	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
798	10727	20567	1.15	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2081	11971	21865	1.56	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4088	13988	23765	2.63	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
7412	17279	27488	3.28	7.0E-60	H58041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
8671	18559	28843	1.96	7.0E-60	H58041.1	EST_HUMAN	yr12f04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element ;
6914	16792		7.13	6.0E-60	H52456.1	EST_HUMAN	yq78h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element ;
78	10062	19878	1.94	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
78	10062	19879	1.94	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2188	12075	21979	0.93	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2188	12075	21980	0.93	4.0E-60	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2942	12869		1.12	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
1815	11712	21591	4.85	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1815	11712	21592	4.85	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1826	11723		2.22	3.0E-60	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
4354	14250	24035	2.08	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
5463	15383	25443	2.06	3.0E-60	AW836198.1	EST_HUMAN	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA
6153	15111	24876	1.31	3.0E-60	AI792814.1	EST_HUMAN	al60h11.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE P52624 URIDINE PHOSPHORYLASE ;
6896	16775	26968	5.4	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6896	16775	26969	5.4	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6990	16867	27061	2.59	3.0E-60	AI040235.1	EST_HUMAN	ox56d09.x1 Soares_NhHMPu_S1 Homo sapiens *cDNA clone* IMAGE:1660337 3' similar to SW:FORM_MOUSE Q05860 FORMIN ;
7077	16954	27147	4.7	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
7569	17420	27637	3.84	3.0E-60	BF102612.1	EST_HUMAN	601646227F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3930990 5'
28	10015	19810	1.79	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1405	11310	21171	2.89	2.0E-60	Z11694.1	NT	H.sapiens 41kDa protein kinase related to rat ERK2
1691	11593	21462	1.29	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3839	13750	23543	0.78	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5910	15816	25941	1.57	2.0E-60	AF004877.1	NT	*Homo sapiens pro-alpha 2(I) collagen* (COL1A2) gene, complete cds
6093	15103	24880	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6093	15103	24881	2.44	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6222	16088	26238	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
6222	16088	26239	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prothymosin, alpha
7145	17022	27216	3.86	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7732	17582	27806	1.89	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
7732	17582	27807	1.89	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
9509	19123		2.86	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
9639	19573		1.31	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
9641	19209		1.46	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC63504), mRNA
9658	19220		1.47	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9957	19420	25169	1.4	2.0E-60	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
511	10453	20264	1.56	1.0E-60	BE178586.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
3827	13739	23531	1.12	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
4874	14754	24533	1.1	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7086	16963		2.9	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.t1 L1 repetitive element ;
7101	16978	27170	1.58	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1083	10999	20840	1.9	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2635	12502	22395	1.39	8.0E-61	AW006478.1	EST_HUMAN	wt05b10.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506555 3'
2635	12502	22396	1.39	8.0E-61	AW006478.1	EST_HUMAN	wt05b10.x1 NCI_CGAP_Co3 *Homo sapiens cDNA clone* IMAGE:2506555 3'
2921	12848		1.74	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)

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Table 4.

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
122	10098	19918	0.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
122	10098	19919	0.94	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10098	19918	0.86	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10098	19919	0.86	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	10230	20045	2	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
794	10723	20564	1.69	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1299	11206	21060	10.28	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1612	11516	21376	0.95	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1628	11532	21392	2.12	6.0E-61	AA596033.1	EST_HUMAN	nn66h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3266	13189	22987	8.19	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5674	15583	25684	2.92	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b {alternatively spliced} [human, B cells, mRNA Partial, 375 nt]
6344	16207	26370	1.93	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
6492	16351	26521	2.03	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-I (GTF2I) mRNA, complete cds
9417	10723	20564	1.43	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1655	11558	21421	1.78	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3000	12928	22720	1.92	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3114	13039	22835	0.84	5.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3161	13086	22890	1.9	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3899	13809		1.68	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
9213	18941		2.76	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
4119	14019	23797	1.13	3.0E-61	BE396279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'
490	10433	20246	1.5	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1194	11104	20950	1.35	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1194	11104	20951	1.35	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1642	11546	21407	1.31	2.0E-61	N53039.1	EST_HUMAN	yv53d11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
2109	11998	21897	1.41	2.0E-61	4758003	NT	Homo sapiens calmegin (CLGN), mRNA
2604	12472		1.16	2.0E-61	N39397.1	EST_HUMAN	yy03f11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270189 5'
5871	15777	25896	1.7	2.0E-61	11426166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6N1A), mRNA
7212	17089	27279	1.33	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG06 5'
7707	17557	27783	1.62	2.0E-61	AW500256.1	EST_HUMAN	UI-HF-BN0-akd-f-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
7885	17735	27979	3.09	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8258	18138		7.14	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
428	10373		0.85	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
756	10686	20524	1.32	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1377	11283	21138	1.09	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1731	11632		0.97	1.0E-61	U32657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1814	11711	21590	4.47	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2150	12038	21935	1.49	1.0E-61	AW827281.1	EST_HUMAN	xn11b09.y1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element MSR1 repetitive element ;
2804	12734	22533	1.67	1.0E-61	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3330	13250	23055	0.88	1.0E-61	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3671	13685	23372	1.47	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
4339	14236	24019	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4339	14236	24020	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4751	14636	24422	7.63	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4751	14636	24423	7.63	1.0E-61	AW298181.1	EST_HUMAN	UI-H-BW0-ajt-b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4878	14758	24535	0.85	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6124	15971	26107	7.19	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds
6268	16133	26287	1.4	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
6268	16133	26288	1.4	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
6729	16609	26800	3.38	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
6838	16717	26910	3.59	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
7348	17216		2.79	1.0E-61	AW999726.1	EST_HUMAN	MR0-BN0070-040400-010-h01 BN0070 Homo sapiens cDNA
7763	17613	27840	6.28	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
8031	17923	28169	1.96	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
9110	19631		1.26	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9149	19620	25002	2.96	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9149	19620	25003	2.96	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9515	19128	25261	1.8	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
9805	19317	25205	8.25	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
4451	14345	24138	0.79	8.0E-62	AA830420.1	EST_HUMAN	oc66h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN ;
9953	19417		1.56	8.0E-62	AA768861.1	EST_HUMAN	nz75g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301328 3'
1091	11007	20848	1.27	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3462	13378	23184	0.79	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
8657	18546	28829	4	7.0E-62	AI208681.1	EST_HUMAN	qg56a04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN. ;
2969	12896		1.07	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3338	13258		3.93	6.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
6496	16355	26525	3.33	6.0E-62	AI762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6496	16355	26526	3.33	6.0E-62	AI762801.1	EST_HUMAN	wi04d02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
6804	16683	26873	1.4	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
7386	17255	27460	2.76	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-a09 ST0203 Homo sapiens cDNA
410	10356	20183	1.49	5.0E-62	AI950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;contains element MER22 repetitive element ;
2356	12236	22132	3.26	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
2356	12236	22133	3.26	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
3372	13291	23090	2.17	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4233	14131	23907	1.65	5.0E-62	AA431093.1	EST_HUMAN	zw78e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT P47245 NARDILYSIN ;
7482	17352	27556	6.17	5.0E-62	AW410687.1	EST_HUMAN	fh07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961616 5'
8587	18455	28723	4.91	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
8587	18455	28724	4.91	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
822	10750	20597	3.47	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
822	10750	20598	3.47	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
823	10750	20597	4.63	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
823	10750	20598	4.63	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1446	11351		0.89	4.0E-62	AA311281.1	EST_HUMAN	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
2409	12286	22183	1.39	4.0E-62	AI827900.1	EST_HUMAN	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
2409	12286	22184	1.39	4.0E-62	AI827900.1	EST_HUMAN	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to gb:X57138_ma1 HISTONE H2B.2 (HUMAN);
3353	13273		6.6	4.0E-62	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4947	14824		2.03	4.0E-62	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5609	15524	25606	1.66	4.0E-62	4506978	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
5804	16709	25822	2.42	4.0E-62	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
6254	16120	26273	1.68	4.0E-62	11421041	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
6498	16357	26528	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6498	16357	26529	2.21	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
7134	17011	27204	6.3	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
8377	18254	28505	2.43	4.0E-62	Z78766.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
8377	18254	28506	2.43	4.0E-62	Z78766.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
9135	18891	28792	2.95	4.0E-62	11418086	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
9355	19578		2.98	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
9743	19305	25201	1.99	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9792	19302	25198	4.2	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9792	19302	25199	4.2	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9835	19335	25210	1.51	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
68	10053	19868	1.12	3.0E-62	4557794	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2) mRNA
3008	12936	22728	0.95	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3008	12936	22729	0.95	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3640	13554	23340	1.92	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
6969	16846	27038	4.35	3.0E-62	AI632733.1	EST_HUMAN	wa33f04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.t2 THR repetitive element ;
1211	11120	20969	1.5	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7096	16973	27165	4.8	2.0E-62	BF329911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
7096	16973	27166	4.8	2.0E-62	BF329911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
7846	17696		3.94	2.0E-62	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8936	18744		8.93	2.0E-62	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
1028	10946	20791	1.24	1.0E-62	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1526	11431	21288	6.83	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1758	11657	21528	1.02	1.0E-62	AA625207.1	EST_HUMAN	af70e11.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453 ;
2884	12811	22606	1.12	1.0E-62	AL039044.1	EST_HUMAN	DKFZp566F104_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566F104 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4426	14321	24108	1.32	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6236	16102	26251	2.17	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
6236	16102	26252	2.17	1.0E-62	AA722878.1	EST_HUMAN	zg89f10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7239	17116	27310	1.53	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
7239	17116	27311	1.53	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
7262	17139	27331	1.81	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
7262	17139	27332	1.81	1.0E-62	X15533.1	NT	H.sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
7512	17300	27507	2.81	1.0E-62	AA485170.1	EST_HUMAN	aa33d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
8673	18561	28845	2.13	1.0E-62	Z78698.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
9623	19199		1.94	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9815	19322	25206	2.3	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
335	10294	20109	2.14	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2297	12179		1.51	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558C10 5'
3955	13863	23638	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
3955	13863	23639	7.42	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5210	15088	29106	6.51	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5354	15274	25104	1.31	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PkB kinase
6262	16127	26281	4.39	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
6845	16724	26917	1.37	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
2296	12178	22077	1.52	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2322	12203	22102	2.17	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3415	13332	23134	3.81	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3415	13332	23135	3.81	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4168	14068	23843	3.37	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
913	10837		1.78	7.0E-63	AI872137.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2439908 3'
5274	15196		40.61	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN);
3279	13200	23001	0.98	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5879	15785	25905	2.86	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
5879	15785	25906	2.86	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
8474	18347	28611	2	4.0E-63	AW134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
8474	18347	28612	2	4.0E-63	AW134709.1	EST_HUMAN	UI-H-BI1-abq-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1893	11788	21666	1.97	3.0E-63	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2753	12615	22506	1.34	3.0E-63	J00310.1	NT	Human Met-tRNA-i gene 1
2791	11127	20978	8.97	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA
5896	15802	25926	27.69	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
7597	17448	27663	1.82	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
7597	17448	27664	1.82	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
184	10156	19972	1.11	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
191	10163	19980	1.74	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
489	10432		1.39	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
809	10738	20583	5.29	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1647	11452	21312	2.47	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1547	11452	21313	2.47	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
3119	13044	22841	1.68	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3248	13171	22970	1.78	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3831	13743	23535	1.86	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4760	14645	24434	1.13	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5587	15502	25578	2.45	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
5587	15502	25579	2.45	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6025	15929	26061	1.37	2.0E-63	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6208	15968	26103	1.41	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6208	15968	26104	1.41	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6964	16842	27034	3.8	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8129	18017	28265	12.54	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
8154	18042	28292	3.02	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
8154	18042	28293	3.02	2.0E-63	AF099810.1	NT	Homo sapiens neurexin III-alpha gene, partial cds
9243	19523	25058	10.85	2.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
9864	19354	25186	1.39	2.0E-63	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
4246	14145	23918	2.91	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4246	14145	23919	2.91	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5526	15443	25509	1.39	1.0E-63	AW582266.1	EST_HUMAN	QV0-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA
6935	16813		2.3	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9879	19633		3.02	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6591	16471	26661	4.78	9.0E-64	AI478186.1	EST_HUMAN	tm50b07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1030	10948		7.89	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
5733	15641	25747	3.16	8.0E-64	BE885755.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
9059	18841		2.61	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9111	18875		2.56	8.0E-64	T60651.1	EST_HUMAN	yb98b02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3486	13402		0.99	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4625	14613	24303	2.44	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4625	14513	24304	2.44	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7766	17616	27844	2.13	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
1692	11594	21463	1.7	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1692	11594	21464	1.7	6.0E-64	AI651992.1	EST_HUMAN	wb51e07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3084	13011	22801	3.7	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3084	13011	22802	3.7	6.0E-64	AW026445.1	EST_HUMAN	wv13e03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
5454	15375	25433	2.64	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5454	15375	25434	2.64	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5464	15384	25444	4.41	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6293	16157	26312	2.58	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6293	16157	26313	2.58	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7376	17245	27451	7.8	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
7472	17332	27538	2.06	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
7604	17455	27669	2.34	6.0E-64	S76475.1	NT	trkC [human, brain, mRNA, 2715 nt]
8151	18039	28287	7.57	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
8151	18039	28288	7.57	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
9262	18967	25321	4.06	6.0E-64	11526198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
803	10732	20574	2.44	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	10732	20575	2.44	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1402	11307	21167	2.42	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1402	11307	21168	2.42	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1683	11585	21457	1.67	5.0E-64	U89358.1	NT	Human l(3)mbt protein homolog mRNA, complete cds
2796	11370	21235	2.66	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2796	11370	21236	2.66	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3876	13787	23575	5.61	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
8188	18074	28324	3.9	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
8188	18074	28325	3.9	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2151	12039	21936	3.85	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-569E02 5'
3216	13140	22943	0.95	3.0E-64	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3396	13313	23112	1.51	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3396	13313	23113	1.51	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
5703	15611	25713	1.34	3.0E-64	Z26273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
5911	15817	25942	3.39	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6933	16811	27005	1.81	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6933	16811	27006	1.81	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
6946	16824	27016	1.3	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
6946	16824	27017	1.3	3.0E-64	BE206521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7422	17289	27497	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7422	17289	27498	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8565	18434	28703	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8565	18434	28704	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8938	18746	29040	4.59	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1072	10988	20831	0.94	2.0E-64	AA609940.1	EST_HUMAN	af09d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1376	11282	21137	1.32	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2478	12354		1.78	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element ;
2484	12359	22252	3.03	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2484	12359	22253	3.03	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3101	13027	22823	2.56	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3719	13631	23416	1.33	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
3719	13631	23417	1.33	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequences, MAGE Homo sapiens cDNA
5653	15565	25662	2.62	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5783	15689	25799	1.3	2.0E-64	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
5906	15812	25938	4.97	2.0E-64	BF668537.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
5976	15880	26004	1.31	2.0E-64	AI078387.1	EST_HUMAN	oz29b03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676717 3'
6024	15928	26060	3.86	2.0E-64	M77185.1	NT	H.sapiens dopamine receptor D5 pseudogene 1, partial cds
8144	18032	28279	2.85	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
8406	18282	28534	6.4	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452211 3'
8406	18282	28535	6.4	2.0E-64	AI922911.1	EST_HUMAN	wn81b06.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452211 3'
9182	18921	25347	1.73	2.0E-64	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9617	19195		2.68	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
258	10224	20039	1.74	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1740	11641	21508	5.88	1.0E-64	AI929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:L21696_cds1 PROTHYMOSIN ALPHA (HUMAN);contains element MSR1 repetitive element ;
3466	13382	23188	5.61	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3536	13452	23248	1.32	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3636	13452	23249	1.32	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
9154	18904		1.62	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2230	12115	22017	0.93	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2230	12116	22018	0.93	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
8822	18635		15.1	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081199-017-e03 BT0257 Homo sapiens cDNA
8799	18613	28903	10.83	8.0E-65	AI929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21. ;
7841	17691	27936	2.05	7.0E-65	BE081653.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1040	10958	20801	1.52	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC06 5'
1880	11776		8.32	6.0E-65	AA550929.1	EST_HUMAN	nj86d10.s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
7080	16957	27150	2.52	6.0E-65	AW083252.1	EST_HUMAN	xc07b09.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORF'S. ;contains L1.b2 L1 repetitive element ;
7209	17086	27275	4.25	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
7209	17086	27276	4.25	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
8247	18127	28375	6.18	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
8787	18602	28892	4.76	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
615	10551	20362	0.91	5.0E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1331	11238	21094	1.62	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1331	11238	21095	1.62	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2110	11899	21898	1.02	5.0E-65	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3217	13141	22944	1.91	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3217	13141	22945	1.91	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
186	10158	19975	1.09	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
728	10660	20491	1.56	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
728	10660	20492	1.56	4.0E-65	AI266468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1062	10978	20822	1.88	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1470	11376	21240	8.28	4.0E-65	4506636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2288	12171	22068	1.03	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2288	12171	22069	1.03	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
5138	15005	24775	0.95	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA
5138	15005	24776	0.95	4.0E-65	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA
5740	15648	25754	3.93	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
5740	15648	25755	3.93	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6285	16149	26304	2.29	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
8020	17870		2.17	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8446	18320	28579	7.47	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
9471	10978	20822	1.34	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
9975	19434	25152	1.58	4.0E-65	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
1212	12646		6.37	3.0E-65	X78932.1	NT	H.sapiens HZF9 mRNA for zinc finger protein
1780	11679	21557	1.14	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
3239	13162	22962	1.39	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3660	13574	23361	0.98	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element ;
4551	14444	24228	1.41	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
7793	17643	27876	1.43	3.0E-65	BE787366.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8693	17877	28119	9.69	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3358	13277	23078	5.27	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
5938	15843		4.55	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
6233	16099	26247	23.12	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
7133	17010	27202	1.27	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
7133	17010	27203	1.27	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
8048	17939	28189	2.85	2.0E-65	11419247	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
9109	18874		4.15	2.0E-65	AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus
9580	19504		2.37	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
85	10069		1.06	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
528	10470	20282	1.32	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
1994	11888	21781	0.91	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3326	13246	23052	0.89	1.0E-65	BE466681.1	EST_HUMAN	hz24a09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3'
3917	13826	23606	2.13	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
3917	13826	23607	2.13	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4112	14012	23789	2.37	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4112	14012	23790	2.37	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
6802	16681	26870	1.58	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
6802	16681	26871	1.58	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
6842	16721	26914	2.38	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
6842	16721	26915	2.38	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
7132	17009	27201	1.76	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
7215	17092	27282	1.62	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
7215	17092	27283	1.62	1.0E-65	AU129040.1	EST_HUMAN	AU129040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
7222	17099		2.83	1.0E-65	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
7456	17265	27469	6	1.0E-65	AI191716.1	EST_HUMAN	qd56a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M29581 ZINC FINGER PROTEIN 8 (HUMAN);contains MER19.t1 MER19 repetitive element ;
7687	17537	27763	1.25	1.0E-65	AU153793.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
8042	17933	28181	2.23	1.0E-65	M26167.1	NT	Human platelet factor 4 varation 1 (PF4var1) gene, complete cds
8158	18046	28298	12.99	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
8473	18346	28610	2.18	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'

Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8542	18414	28681	2.35	1.0E-65	AI621017.1	EST_HUMAN	ts76a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_rna1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
9155	18905		2.27	1.0E-65	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
9254	18963	25318	4.85	1.0E-65	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9665	19225		1.44	1.0E-65	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
65	10051	19864	1.51	9.0E-66	AL160311.1	NT	Novel human gene mapping to chomosome 22
65	10051	19865	1.51	9.0E-66	AL160311.1	NT	Novel human gene mapping to chomosome 22
1332	11239	21096	2.49	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1332	11239	21097	2.49	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1468	11373		4.18	9.0E-66	M87299.1	NT	Human transposon-like element, partial
3826	13738	23529	0.9	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3826	13738	23530	0.9	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4591	14479	24266	0.88	8.0E-66	AA424304.1	EST_HUMAN	zv90c05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767048 5'
8654	18543		1.73	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4269	14168	23944	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
4269	14168	23945	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
4269	14168	23946	1.22	6.0E-66	AI924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A CE18595 ;
8499	18372	28636	7.07	6.0E-66	X69181.1	NT	H.sapiens mRNA for ribosomal protein L31
1344	11250	21107	2.25	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
7357	17225	27424	12.31	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
773	10703	20542	0.79	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2235	12120	22022	1.94	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2425	12302		3.66	4.0E-66	AJ223364.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4674	14560		5.15	4.0E-66	9635487	NT	Human endogenous retrovirus, complete genome
5407	15326	25376	3.35	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5512	15430	25494	1.78	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6096	15106	24869	4.71	4.0E-66	AW965473.1	EST_HUMAN	EST377546 MAGE resequences, MAGI Homo sapiens cDNA
6232	16098	26246	6.89	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
6708	16588	26776	6.38	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8052	17943	28193	1.96	4.0E-66	BF507493.1	EST_HUMAN	UI-H-BW1-amr-a-10-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
1408	11313	21175	24.62	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1408	11313	21176	24.62	3.0E-66	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1939	11834	21717	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
1939	11834	21718	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
1939	11834	21719	0.84	3.0E-66	N55323.1	EST_HUMAN	yz27g12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1/H2B.2. [2] PIR:B56612 ;
2675	12540	22430	2.91	3.0E-66	11141880	NT	Homo sapiens TGF(beta)-induced transcription factor 2 (TGIF2), mRNA
3079	13006	22797	5.47	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5528	15445	25511	1.64	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6528	15445	25512	1.64	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8800	18614	28904	8.3	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
45	10033	19837	1.02	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
45	10033	19838	1.02	2.0E-66	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
416	9983	19774	0.93	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
416	9983	19775	0.93	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1784	11682	21560	2.02	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2944	12871	22669	0.95	2.0E-66	X65859.1	NT	H.sapiens pseudogene for the low affinity IL-8 receptor
3975	13882	23657	0.86	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4556	14448	24233	12.69	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4556	14448	24234	12.69	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
7135	17012	27205	2.16	2.0E-66	N45480.1	EST_HUMAN	yy59c02.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:277826 5'
9475	19712		2.22	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
2864	12792	22585	1.38	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2864	12792	22586	1.38	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4288	12792	22585	3.26	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4288	12792	22586	3.26	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession . No.	Top Hit Database Source	Top Hit Descriptor
5306	15227	25031	5.36	1.0E-66	BF673088.1	EST_HUMAN	602152996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
6143	15991	26126	1.49	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G06 BN0193 Homo sapiens cDNA
6926	16804	26998	1.37	1.0E-66	AA668858.1	EST_HUMAN	aa80e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827262 3'
8312	18189	28438	2.39	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9260	18965		2.09	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4829	14711		0.84	8.0E-67	M78158.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPN31 similar to L1 repetitive element
376	10360	20184	6.19	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1360	11266	21122	2.63	7.0E-67	AA383416.1	EST_HUMAN	EST96812 Testis I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1535	11439	21296	1	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1536	11439	21297	1	7.0E-67	W85947.1	EST_HUMAN	zh56b05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1988	11881	21773	1.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
1988	11881	21774	1.06	7.0E-67	7657243	NT	Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
2779	10360	20184	7.07	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5793	15699	25807	2.04	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
5793	15699	25808	2.04	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9039	18826	29111	1.56	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9039	18826	29112	1.56	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9501	19116	25292	3.33	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9868	19357		1.43	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
647	10488	20297	1.32	6.0E-67	X68968.1	NT	H.sapiens mRNA for acetyl-CoA carboxylase
778	10708	20547	1.5	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmebrane receptor protein
1252	11159	21008	0.93	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3131	13056	22856	1.24	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3391	13308	23106	1.2	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3391	13308	23107	1.2	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4035	13938	23714	1.28	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4035	13938	23715	1.28	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4607	14495	24283	3.37	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4607	14495	24284	3.37	6.0E-67	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5125	14761		2.1	6.0E-67	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3184	13109	22913	2.45	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8352	18229		2.1	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1306	11213	21069	1.83	4.0E-67	R90819.1	EST_HUMAN	yn02d11.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
6883	16762		1.22	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-150900-026-c03 HT0934 Homo sapiens cDNA
8416	18290		2.3	4.0E-67	AA714294.1	EST_HUMAN	nw06a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385 PRO-POL-DUTPASE POLYPROTEIN ;
2782	10553	20365	0.93	3.0E-67	AA333768.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
3407	13324	23125	1.14	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4596	14484	24270	3.14	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
6760	16639	26827	1.22	3.0E-67	BF196068.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1 ;
8583	18451		19.27	3.0E-67	AA927874.1	EST_HUMAN	om18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
180	10152	19967	1.94	2.0E-67	BE348354.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9 CE09617 ;
827	10754	20604	6	2.0E-67	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
1089	11005		1.74	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
1841	11737	21614	1.5	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
1841	11737	21615	1.5	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:O94892 O94892 KIAA0798 PROTEIN. ;
2336	12216	22116	0.98	2.0E-67	AF309561.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2381	12261	22153	1.2	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3422	13339	23144	3.9	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
3921	13830	23610	2.33	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5724	15631	25734	4.22	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
5803	15708	25820	2.17	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
5803	15708	25821	2.17	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
7202	17079	27264	1.34	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
7202	17079	27265	1.34	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
8409	19769		3.26	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8558	18428	28698	1.77	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
8751	17900	28144	2.26	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
9388	19577	25069	2.6	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
253	10219	20036	4.37	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2129	12017	21915	2.46	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3794	13706	23492	4.96	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;
3794	13706	23493	4.96	8.0E-68	AA209456.1	EST_HUMAN	zq82h10.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN. ;
1849	11745		2.2	6.0E-68	AW503842.1	EST_HUMAN	UI-HF-BN0-alb-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078924 5'
7971	17821	28064	2.46	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
8489	18362	28627	1.93	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9676	19234		1.42	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
9918	19391	25178	1.36	6.0E-68	BF310675.1	EST_HUMAN	601894635F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
785	12642	20555	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
785	12642	20556	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
802	10731	20572	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
802	10731	20573	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3108	13034	22830	2.62	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2480	12356	22247	1.01	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2480	12356	22248	1.01	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4900	14780		17.24	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6061	16044	26188	5.64	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6061	16044	26189	5.64	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7225	17102	27290	5.41	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7225	17102	27291	5.41	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7295	17171	27371	2.39	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
3611	13525	23312	5.61	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
7441	16454		4.44	3.0E-68	AI342323.1	EST_HUMAN	qt38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR.t2 THR repetitive element ;
7997	17847	28088	1.45	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
9872	19502		1.53	3.0E-68	AW939485.1	EST_HUMAN	QV1-DT0072-010200-056-h06 DT0072 Homo sapiens cDNA
2832	15076		12.26	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4583	14473	24261	1.66	2.0E-68	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6110	16004		8	2.0E-68	R45088.1	EST_HUMAN	yg38g04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6202	15962	26095	4.79	2.0E-68	BF035316.1	EST_HUMAN	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
9148	19731		.1.92	2.0E-68	BE897376.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
72	10056	19873	1.31	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
293	10257	20078	9.36	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2205	12092	21994	1.32	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2205	12092	21995	1.32	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2728	12590	22486	1.01	1.0E-68	AW451832.1	EST_HUMAN	UI-H-BI3-alk-f-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
3928	13837	23617	0.95	1.0E-68	BE296032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
4954	14831	24598	0.98	1.0E-68	AA897343.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5261	15183	24959	1.57	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8226	18108	28361	2.44	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
8226	18108	28362	2.44	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
8275	18155	28396	2.29	1.0E-68	L76416.1	NT	Homo sapiens MIF2 suppressor (HSMT3) mRNA, complete cds
9659	10056	19873	1.95	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9862	19669	24991	1.38	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
19	10006	19797	1.82	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
19	10006	19798	1.82	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1011	10929	20772	1.63	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1011	10929	20773	1.63	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4037	13940	23718	0.78	9.0E-69	4757867	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
8263	18143		9.27	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3340	13260		1.21	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
5834	15740	25852	6.08	7.0E-69	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
6589	16469	26659	3.61	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
6589	16469	26660	3.61	6.0E-69	AI192764.1	EST_HUMAN	qe62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gb:L11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
509	10451		1.88	4.0E-69	AI873630.1	EST_HUMAN	wm26h11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2437125 3'
5566	15481	25554	4.12	4.0E-69	AI764973.1	EST_HUMAN	wh57b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137 O55137 ACYL-COA THIOESTERASE. ;
5995	15900	26024	2.43	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
5995	15900	26025	2.43	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
380	10364	20187	2.81	3.0E-69	BE258012.1	EST_HUMAN	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
596	10532	20340	1.64	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1536	11440		1.35	3.0E-69	T80514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP:A48836 A48836 SPEGF III=EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN ;
2325	12206		0.88	3.0E-69	5729910	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
3990	13897	23674	0.86	3.0E-69	AI765888.1	EST_HUMAN	wh66g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
5209	15087	29105	5.94	3.0E-69	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6387	16249	26410	1.37	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
6457	16318	26485	8.43	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
7091	16968		1.26	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
7417	17284	27491	1.54	3.0E-69	X13223.1	NT	H.sapiens mRNA for N-acetylglucosamide-(beta 1-4)-galactosyltransferase
7493	17363	27568	2.24	3.0E-69	X06233.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
8036	17928	28174	3.07	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
8215	18099		7.12	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
9168	18911		4.13	3.0E-69	11419157	NT	Homo sapiens HGC6.2 protein (HGC6.2), mRNA
124	10344	20170	1	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
124	10344	20171	1	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
398	10344	20170	4.94	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
398	10344	20171	4.94	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alphaIIb protein gene, partial cds
1842	11738	21616	1.2	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2813	12742		2.73	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
1675	11577	21445	2.35	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5981	15886	26008	3.68	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6080	16063	26211	1.55	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6080	16063	26212	1.55	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6088	16033	26173	2.93	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6088	16033	26174	2.93	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7847	17697	27942	5.29	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
7847	17697	27943	5.29	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
8246	18126		23.27	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
9105	18872	28785	1.53	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9510	19124		2.32	1.0E-69	AI809994.1	EST_HUMAN	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360390 3' similar to contains Alu repetitive element;contains element MIR repetitive element ;
2284	12717	22065	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008023
4277	14176	23954	2.16	8.0E-70	L77566.1	NT	Homo sapiens DGS-I mRNA, 3' end
1771	11670	21547	1.93	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1771	11670	21548	1.93	7.0E-70	AI497807.1	EST_HUMAN	tm89f01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2165305 3'
1888	11784	21660	1.63	7.0E-70	AA282955.1	EST_HUMAN	zt15h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2018	11909		3.57	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4132	14032	23807	3.86	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5369	15289	25124	5.28	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5369	15289	25125	5.28	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6138	15985	26120	1.89	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
6910	16788	26980	2.36	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
6910	16788	26981	2.36	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
7063	16940	27131	3.98	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
7063	16940	27132	3.98	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
7283	17159	27357	3.72	7.0E-70	X59841.1	NT	Human PBX3 mRNA
7283	17159	27358	3.72	7.0E-70	X59841.1	NT	Human PBX3 mRNA
7428	16441	26627	3.13	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
7445	16457	26648	1.56	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
7445	16457	26649	1.56	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
8875	18687	28978	1.78	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
8875	18687	28979	1.78	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
853	10780	20630	1.93	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2090	11979	21874	1.36	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2461	12338	22232	0.99	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2505	12723	22268	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2505	12723	22269	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
9116	18879		1.73	5.0E-70	BE166034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
1571	11475	21332	0.89	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA
1571	11475	21333	0.89	3.0E-70	BE071796.1	EST_HUMAN	RC0-BT0522-071299-011-a12 BT0522 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5845	15751	25865	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
5845	15751	25866	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
674	10608	20426	13.15	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
674	10608	20427	13.15	2.0E-70	N42161.1	EST_HUMAN	yy07a10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
689	10622	20449	2.01	2.0E-70	AI246899.1	EST_HUMAN	qx51h01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1004	10922	20766	1.7	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1167	11079	20924	1.95	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1167	11079	20925	1.95	2.0E-70	7661983	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1387	11292	21148	0.97	2.0E-70	BE467311.1	EST_HUMAN	hz64c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
1708	11609	21479	2.09	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2272	12166		3.62	2.0E-70	AA054010.1	EST_HUMAN	zf48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A P03345 GAG POLYPROTEIN ;
3963	13870	23648	3.95	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5385	15304	25156	8.05	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS8)
5385	15304	25157	8.05	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS8)
5766	15673	25780	1.42	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
5999	15904	26028	1.88	2.0E-70	D12625.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6010	15915	26042	9.83	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6010	15915	26043	9.83	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6177	15134	24853	1.69	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetyllacosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
6618	16498	26685	7.67	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
7835	17685	27930	1.3	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
8422	18296	28550	3.19	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8422	18296	28551	3.19	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8908	18716	29010	5.82	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
9499	19114	25289	2.58	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9499	19114	25290	2.58	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3347	13267		2.97	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
7642	17492		2.57	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
8305	18182	28429	13.73	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLBGB10 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5621	15536	25621	6.04	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE. ;
5621	15536	25622	6.04	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045 O14045 PHOSPHOTRANSFERASE. ;
6192	16077	26226	1.88	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
8811	16077	26226	4.65	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
7245	17122		1.97	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL ;
6363	16226	26386	7.91	7.0E-71	AA442230.1	EST_HUMAN	zv60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
7037	16914	27103	1.52	7.0E-71	AA705457.1	EST_HUMAN	zj91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
8643	18507	28786	4.18	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2163	12050	21951	3.45	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4030	13933	23710	1.38	5.0E-71	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
5144	15011	24782	3.2	5.0E-71	AI829496.1	EST_HUMAN	wl18h10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2425315 3'
5586	15501	25577	2.14	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6434	16295	26457	1.59	5.0E-71	M38106.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
6548	16406	26585	19.78	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
7702	17552		2.26	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
8348	18225	28477	1.9	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
8528	18400	28668	2	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63326), mRNA
9067	18848	29116	1.84	5.0E-71	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9411	19063		1.62	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
97	10082	19899	1.13	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
347	10306	20123	115.63	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	10306	20124	115.63	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	12778	22566	0.88	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2850	12778	22567	0.88	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2857	12785	22575	1.63	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4330	14227	24009	3.35	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4913	14792	24567	4.99	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8077	17968	28218	3.32	3.0E-71	AA557683.1	EST_HUMAN	nl45h10.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.t3 PTR5 repetitive element ;
1210	11119	20968	2.52	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5259	15181	24957	6.96	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5259	15181	24958	6.96	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
8022	17872	28114	2.56	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8022	17872	28115	2.56	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8079	17970	28219	2.3	2.0E-71	BE018477.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
9181	18920		6.22	2.0E-71	T95489.1	EST_HUMAN	ye43e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
622	10559	20371	2.11	1.0E-71	AI077927.1	EST_HUMAN	oy15e03.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element ;
926	10851	20699	1.93	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1084	11000	20841	4.01	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1317	11224	21080	10.59	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
2036	11927	21821	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2036	11927	21822	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2661	12528	22416	4.85	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3457	13373	23179	1.17	1.0E-71	AF119665.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3546	13462	23256	4.73	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3546	13462	23257	4.73	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3597	13511	23298	0.94	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3597	13511	23299	0.94	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3681	13595	23381	1.87	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 19
4370	14266	24050	1.86	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
6044	15947	26079	1.4	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
6326	16189	26351	10.62	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
6750	16629	26816	6.96	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
6916	16794	26986	4.18	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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6916	16794	26987	4.18	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
7748	17598	27820	6.49	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
7792	17642		3.39	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
8164	18052		4.87	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
8256	18136	28383	3.2	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
8486	18359	28623	2.33	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
8486	18359	28624	2.33	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
9547	19147		4.48	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
401	10347	20173	1.15	9.0E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element;
401	10347	20174	1.15	9.0E-72	AI857635.1	EST_HUMAN	wk95g03.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705 HYPOTHETICAL 38.6 KD PROTEIN. ;contains Alu repetitive element;
4023	13926	23700	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
4023	13926	23701	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
4023	13926	23702	5.23	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitocondrial protein, mRNA
6228	16094	26244	2.94	7.0E-72	S41694.1	NT	{pseudogene} PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
6885	16764		3.72	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8788	18603	28893	2.22	6.0E-72	BF059578.1	EST_HUMAN	7k63a05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480080 3' similar to SW:KMLC_RABIT P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE ;
56	10043	19854	0.88	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
56	10043	19855	0.88	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
57	10043	19854	2.95	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
57	10043	19855	2.95	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-e11 CS0010 Homo sapiens cDNA
1122	11037		2.76	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6150	16023	26163	1.47	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
7097	16974	27167	3.55	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN ;contains element MSR1 repetitive element ;
8569	18437	28706	3.18	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
8569	18437	28707	3.18	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
9253	19700		2.43	5.0E-72	BE926645.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4716	14602		1.06	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
6380	16242	26402	1.4	4.0E-72	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
7633	17484	27705	1.42	4.0E-72	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
8815	18628	28917	7.32	4.0E-72	H79421.1	EST_HUMAN	yu28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
8929	18737	29030	2.76	4.0E-72	T81910.1	EST_HUMAN	yd29d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
9603	19185	25249	4.2	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
885	10811		4.88	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1139	11053	20894	6.06	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1139	11053	20895	6.06	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
3037	12965	22759	10.51	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3241	13164	22963	2.63	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3750	13663	23445	2.51	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene {alternatively spliced, splice junction} [human, precursor B-cell line REH, mRNA Partial, 211 nt]
4445	14339	24129	3.22	3.0E-72	11416196	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4836	14717	24600	0.94	3.0E-72	AI654337.1	EST_HUMAN	wb31a08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307254 3'
5639	15552	25643	2.4	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5639	15552	25644	2.4	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5743	15661	25758	4.35	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5743	15651	25759	4.35	3.0E-72	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5988	15893	26016	3.02	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
6475	16334	26501	2.32	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6755	16634	26822	1.26	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
7960	17810	28051	1.3	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
9516	19129	25262	1.85	3.0E-72	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8122	18010	28257	4.45	2.0E-72	AA789277.1	EST_HUMAN	aj28b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);
9600	19182	25246	3.74	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
2030	11921	21812	2.61	1.0E-72	AA846225.1	EST_HUMAN	ai83d02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
5524	15441	25506	3.15	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
5949	15854	25976	19.78	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5949	15854	25977	19.78	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6501	16360	26533	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6501	16360	26534	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7532	17383	27594	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
7532	17383	27595	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1443	11348	21213	1.23	9.0E-73	AW374968.1	EST_HUMAN	MR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA
8320	18197		23.9	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1022	10939	20782	1.03	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q59050 Q59050 HYPOTHETICAL PROTEIN MJ1656. ;
1399	11304	21163	3.06	8.0E-73	AI024877.1	EST_HUMAN	ov39h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639743 3'
5959	15864	25986	4.6	8.0E-73	11426469	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
6715	16595	26785	2	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
7385	17254	27459	15.88	8.0E-73	BE019900.1	EST_HUMAN	bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
7614	17465	27682	2.22	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
7614	17465	27683	2.22	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9446	19081	25282	2.12	8.0E-73	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9654	19217	25235	2.69	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1116	11033	20875	0.78	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3261	13184	22983	1.06	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4863	14743		1.62	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
152	10126		2.37	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
6255	16121	26274	3.36	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5215	15138	24832	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1818	11715	21595	0.99	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1818	11715	21596	0.99	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
833	10760	20610	1.75	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
1902	11798		1.48	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2251	12135		1.1	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3144	13069	22869	3.48	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3503	13420	23221	0.96	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA

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3503	13420	23222	0.96	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
5902	15808	25933	7.6	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6023	15927	26058	1.35	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6023	15927	26059	1.35	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7956	17806	28048	1.34	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
7993	17843	28085	2.45	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
7993	17843	28086	2.45	2.0E-73	11496980	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
8138	18026	28272	4.14	2.0E-73	11431598	NT	Homo sapiens KIAA1080 protein; Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2 (KIAA1080), mRNA
8408	18284	28537	3.79	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
8408	18284	28538	3.79	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
8432	18306	28562	1.78	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
9447	11798		1.72	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1743	11644	21512	1.57	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2434	12311	22207	0.93	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
7469	17329	27534	1.36	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element MER22 repetitive element ;
8747	17896	28140	2.67	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
723	10655	20485	1.39	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
5606	15521	25602	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
5606	15521	25603	1.84	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1906	11801	21679	3.01	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3286	13207	23007	0.99	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7327	17231	27432	2	7.0E-74	BE967432.1	EST_HUMAN	601649284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932997 5'
9653	19216	25234	2.81	7.0E-74	BE266305.1	EST_HUMAN	601191927F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
1106	11022	20865	2.58	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1609	11514	21373	1.03	6.0E-74	AW263177.1	EST_HUMAN	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2268	12152	22050	9.96	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2268	12152	22051	9.96	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2834	12762	22553	1.39	6.0E-74	AW014039.1	EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2834	12762	22554	1.39	6.0E-74	AW014039.1	EST_HUMAN	UI-H-BI0-aah-h-03-0-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3652	13566	23352	2.63	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3652	13566	23353	2.63	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5294	15215	25016	2.49	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
887	10813	20661	2.58	5.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2669	12534		5.19	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5320	15240	25045	2.15	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5539	15456	25526	10.48	5.0E-74	X89670.1	NT	H.sapiens mRNA for TPCR16 protein
5563	15479	25552	6.74	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5602	15516	25594	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
5602	15516	25595	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6120	16014	26152	3.73	5.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6684	16564	26758	2.69	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
8117	18006	28252	1.88	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-I
8117	18006	28253	1.88	5.0E-74	Y09420.1	NT	H.sapiens mRNA for HIP-I
278	10243	20063	1.89	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
834	10761	20611	4.95	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1919	11814	21692	2.44	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1919	11814	21693	2.44	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2027	11918	21808	4.34	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2027	11918	21809	4.34	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2085	11975	21870	1.21	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2377	12257	22149	0.99	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3052	12979	22772	4.44	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3483	13399	23204	0.93	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3973	13880	23655	1.31	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4457	14351	24142	1.57	4.0E-74	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4512	14405	24192	0.82	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmebrane receptor protein
5006	14880	24644	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
5006	14880	24645	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
6977	16854		5.03	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7394	17312	27519	2.42	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPF81
7921	17771	28010	2.22	3.0E-74	AA601493.1	EST_HUMAN	no17g05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
942	10867	20714	126.24	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
942	10867	20715	126.24	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1158	11071	20916	1.01	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1224	11132	20986	1.15	2.0E-74	AI950528.1	EST_HUMAN	wx51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;contains element MER22 repetitive element ;
1577	11481	21340	2.94	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1577	11481	21341	2.94	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2558	12430	22323	1.09	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r tumor2 Homo sapiens cDNA 3'
4937	14815	24582	1.96	2.0E-74	AL355092.1	NT	Novel human gene mapping to chomosome 22
4937	14815	24583	1.95	2.0E-74	AL355092.1	NT	Novel human gene mapping to chomosome 22
4942	14820	24588	1.89	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5543	19446	25530	1.64	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA
5594	19448	25584	1.98	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5594	19448	25585	1.98	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5629	19448	25584	2.57	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5629	19448	25585	2.57	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6219	16085	26235	1.55	2.0E-74	BF030788.1	EST_HUMAN	601557524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
6631	16511	26700	1.43	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
7398	17316	27523	6.54	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9387	19047		1.46	2.0E-74	AA196181.1	EST_HUMAN	zp96a06.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
9903	19380	25196	1.26	2.0E-74	BF666568.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278559 5'
47	10035	19841	0.97	1.0E-74	7657334	NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA
334	10293	20108	3.6	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
491	10434	20247	1.19	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
497	10439	20252	2.7	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
586	10524	20331	1.35	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
983	10906	20751	2.17	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2179	12066	21968	6.19	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3100	13026	22822	5.96	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3887	13798	23584	4.56	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3974	13881	23656	0.9	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-f06 BT0642 Homo sapiens cDNA
4170	14070	23845	0.9	1.0E-74	BE467769.1	EST_HUMAN	hz73h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:B0511.12 CE17351 ;
5112	14980	24754	1.19	1.0E-74	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
6694	16574	26765	1.83	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
6694	16574	26766	1.83	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
7112	16989	27182	3.92	1.0E-74	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
7988	17838	28079	1.31	1.0E-74	11420549	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783), mRNA
9024	18818	29108	1.6	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9106	18873		2.83	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9249	12066	21968	4.14	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9720	19261		1.36	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2607	12475		4.07	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
9406	19059		1.67	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2273	12157	22055	0.88	6.0E-75	AI817415.1	EST_HUMAN	wk38a08.x1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
6128	14995		0.86	6.0E-75	AA789285.1	EST_HUMAN	aj28c06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391626 3' similar to TR:Q15377 Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN ;
5102	14970	24746	1.04	5.0E-75	BE841305.1	EST_HUMAN	MR0-SN0040-080600-006-g06 SN0040 Homo sapiens cDNA
7395	17313	27520	1.22	5.0E-75	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
7876	17726	27969	3.1	5.0E-75	AI638623.1	EST_HUMAN	tt31c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361 HYPOTHETICAL 20.1 KD PROTEIN ;
107	10088	19903	1.05	4.0E-75	BE081333.1	EST_HUMAN	QV1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
451	10395		1.23	4.0E-75	N36757.1	EST_HUMAN	yx90h08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:269055 5'
1728	11629	21498	1.5	4.0E-75	AW897230.1	EST_HUMAN	CM0-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
2818	12747	22540	4.65	4.0E-75	BE409464.1	EST_HUMAN	601303866F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
5792	15698	25806	4.29	4.0E-75	5579457	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (110kD) (EIF3S8), mRNA
6052	15953	26084	1.56	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6052	15953	26085	1.56	4.0E-75	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
8072	17963	28214	8.72	4.0E-75	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
986	10909	20754	2.91	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
987	10909	20754	2.25	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1795	11693	21569	1.98	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2065	11955	21852	1.05	3.0E-75	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
2373	12253	22144	3.66	3.0E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 29kD (SNAP29) mRNA
2988	12916	22711	1.19	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3152	13077	22877	1.33	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3306	13227	23030	1.01	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3306	13227	23031	1.01	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4077	13979	23759	1.42	3.0E-75	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4336	14233	24015	0.96	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
6058	16041	26183	1.53	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6058	16041	26184	1.53	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6234	16100	26248	3.83	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6234	16100	26249	3.83	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6494	16363	26522	2.92	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
6494	16353	26523	2.92	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7193	17070	27259	1.23	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA
5480	15400		1.5	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cdA Homo sapiens cDNA clone cdABED02 5'
7082	16959	27152	1.73	2.0E-75	AI311783.1	EST_HUMAN	qo91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE ;
2255	12139	22037	5.09	1.0E-75	AW168135.1	EST_HUMAN	xg60d02.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.t1 PTR7 repetitive element ;
2916	12843	22644	3.17	1.0E-75	X52221.1	NT	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
6903	16781		4.13	1.0E-75	AA399270.1	EST_HUMAN	zt57h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN);
7423	17290	27499	3.73	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
7423	17290	27500	3.73	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
8257	18137		3.99	1.0E-75	AA664377.1	EST_HUMAN	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
8441	18315	28573	2.6	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9299	15100	24892	1.86	1.0E-75	BE894192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
38	10026	19825	1.45	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
38	10026	19826	1.45	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;
2364	12244		1.16	9.0E-76	AA702415.1	EST_HUMAN	zi85b07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
7697	17547	27770	23.8	9.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
923	10848	20695	1.69	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
923	10848	20696	1.69	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2880	12807	22603	1.06	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
5744	15652	25760	5.38	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
6421	16282	26443	1.3	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8057	17948	28198	6.44	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
9636	19207		1.44	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
759	10689	20527	4.12	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3254	13177	22975	2.64	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3260	13183	22982	7.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3293	13215	23017	1.1	7.0E-76	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4275	14174	23951	4.3	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4275	14174	23952	4.3	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1214	11122		19.65	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
8761	17910	28154	2.69	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1899	11795	21673	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21674	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21675	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
7759	17609	27834	5.6	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
7759	17609	27835	5.6	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFujiwara) Homo sapiens cDNA clone GEN-178G01 5'
613	10549	20359	1.78	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
613	10549	20360	1.78	3.0E-76	BF516262.1	EST_HUMAN	UI-H-BW1-anz-b-04-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1581	11485	21345	2.78	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1581	11485	21346	2.78	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3382	13300	23099	4.18	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3382	13300	23100	4.18	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5204	15084	29104	9.13	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5842	15748	25861	7.85	3.0E-76	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
6737	16616	26806	1.92	3.0E-76	N42671.1	EST_HUMAN	yy20g10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:271842 5'
7602	17453	27667	3.2	3.0E-76	AW299353.1	EST_HUMAN	xs49h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
7615	17466	27684	1.32	3.0E-76	AA442309.1	EST_HUMAN	zv54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
7615	17466	27685	1.32	3.0E-76	AA442309.1	EST_HUMAN	zv54d11.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
9014	19537	25062	2.13	3.0E-76	AW967984.1	EST_HUMAN	EST380059 MAGE resequences, MAGJ Homo sapiens cDNA
9120	19745	24895	3.75	3.0E-76	AW956455.1	EST_HUMAN	EST368525 MAGE resequences, MAGD Homo sapiens cDNA
280	10245	20065	1.22	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	10298	20112	3.66	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
339	10298	20113	3.66	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
453	10397		2.17	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
575	10513	20320	1.07	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1014	10932	20778	1.03	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1518	11423	21281	1.53	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1518	11423	21282	1.53	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1886	11782	21658	1.43	2.0E-76	AA253954.1	EST_HUMAN	zs60h11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2811	12740	22536	2.83	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F6
3257	13180	22979	2.01	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
3257	13180	22980	2.01	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
4043	10245	20065	0.94	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
4867	14747	24527	6.33	2.0E-76	AW879618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5068	14938	24710	1.25	2.0E-76	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
5453	15374	25432	4.74	2.0E-76	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6518	16377	26554	1.79	2.0E-76	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
7898	17748	27988	3.28	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA
8293	18172	28416	2.76	2.0E-76	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
4200	14100	23881	2.18	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4200	14100	23882	2.18	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5345	15266	25093	5.29	1.0E-76	BE796537.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6137	15984	26119	3.98	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
4421	14316	24101	1.65	8.0E-77	BF205181.1	EST_HUMAN	601866926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5347	15268	25095	2.46	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
8691	18578	28861	2.12	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
8691	18578	28862	2.12	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
9771	19289	25232	7.25	8.0E-77	R00245.1	EST_HUMAN	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element ;
1887	11783	21659	3.28	7.0E-77	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2360	12240	22136	2.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2360	12240	22137	2.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
262	10227	20043	4.29	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1125	11040	20882	0.9	6.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1524	11429	21287	17.64	6.0E-77	AI204066.1	EST_HUMAN	qe77h12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1216	11124	20973	1.78	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1337	11243	21101	1.16	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2736	12598	22492	0.97	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
4605	14493	24280	2.02	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4605	14493	24281	2.02	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
4853	14733	24514	2.05	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6873	16752	26947	1.39	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
6873	16752	26948	1.39	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
7519	17338	27543	2.55	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
7519	17338	27544	2.55	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
7990	17840	28080	1.96	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
7990	17840	28081	1.96	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
1929	11824	21705	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1929	11824	21706	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
8249	18129	28377	3.31	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1330	11237	21093	1.71	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1414	11320	21185	1.73	2.0E-77	AW997712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2044	11935	21830	0.84	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2056	11946	21842	2.64	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2549	12724	22312	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2549	12724	22313	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3947	13655	23629	1.33	2.0E-77	BE044316.1	EST_HUMAN	ho43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4315	14212	23995	0.89	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4315	14212	23996	0.89	2.0E-77	AI613519.1	EST_HUMAN	tw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245 O65245 F21E10.7 PROTEIN. ;
4492	14386		3.48	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4659	14546	24334	3.58	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29. [1] ;contains element MSR1 repetitive element ;
5625	15540	25629	1.8	2.0E-77	BE298940.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
5745	15653	25761	1.34	2.0E-77	BE787143.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
6257	16123	26276	12.74	2.0E-77	AI833003.1	EST_HUMAN	at74a09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151. [1] ;
7489	17359	27564	4.99	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
7489	17359	27565	4.99	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
37	10024	19821	0.97	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
37	10024	19822	0.97	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
271	10237	20054	1.87	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
271	10237	20055	1.87	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	12679	20635	4.95	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
857	12679	20636	4.95	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2394	12272	22168	1.22	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3007	12935	22727	2.82	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4256	14155	23930	2.99	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4423	14317	24103	14.73	1.0E-77	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4552	14445	24229	1.95	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5179	15043	24810	2.89	1.0E-77	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5610	15525	25607	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5610	15525	25608	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5688	15597	25698	1.56	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6197	15957	26089	11.39	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
8002	17852	28093	1.22	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
8002	17852	28094	1.22	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds
8013	17863	28109	2.63	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
5880	15786	25907	2.97	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6880	15786	25908	2.97	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
80	10064	19881	1.83	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
80	10064	19882	1.83	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
6950	15855		2.51	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
211	10182	19996	1.1	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2515	12389	22281	4.1	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B6A.6 CE22121 ;
3339	13259	23066	3.81	5.0E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5323	15243	25048	2.39	5.0E-78	AF038536.1	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
5422	15343	25396	9.35	5.0E-78	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
6244	16110	26262	2.17	5.0E-78	AW953120.1	EST_HUMAN	EST365190 MAGE resequences, MAGB Homo sapiens cDNA
7248	17125	27318	6.5	5.0E-78	U60889.1	NT	Human lysosomal alpha-mannosidase (manB) gene, exon 7
7249	17126	27319	3.75	5.0E-78	BE960836.1	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1502	11406	21265	1.6	4.0E-78	AL355841.1	NT	Novel human gene mapping to chomosome 22
1629	11533	21393	1.53	4.0E-78	AI985094.1	EST_HUMAN	wr97b12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2495615 3' similar to SW:WAP_PIG O46655 WHEY ACIDIC PROTEIN PRECURSOR ;
2270	12154	22053	2.21	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4227	14125	23899	1.39	4.0E-78	7656876	NT	Homo sapiens syncytin (LOC30816), mRNA
4664	14550	24340	1.27	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4664	14550	24341	1.27	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
7967	17817	28058	1.94	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7967	17817	28059	1.94	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
8721	18538	28822	1.97	4.0E-78	AF169148.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
8844	18656	28944	3	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
9664	19224	25239	2.85	4.0E-78	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
155	10129	19944	1.6	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
166	10129	19945	1.6	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3178	13103	22908	0.91	3.0E-78	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
4015	13657	23439	0.93	3.0E-78	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
7902	17762		5.56	3.0E-78	BE144758.1	EST_HUMAN	CM0-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
8349	18226	28478	5.52	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
3083	13010		2.22	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3932	13841		1.68	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
6412	16274	26435	1.46	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6412	16274	26436	1.46	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BK0-aaj-g-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6547	16405	26584	3.88	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
6687	16667	26761	2.73	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
6921	16799	26991	1.84	2.0E-78	AI557509.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
6921	16799	26992	1.84	2.0E-78	AI557509.1	EST_HUMAN	Pt2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8429	18303	28559	4.5	2.0E-78	AI197837.1	EST_HUMAN	qi50h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP:R90.1 CE06325 PROTEIN KINASE ;
8467	18340	28605	3.28	2.0E-78	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
5247	15170	24943	2.9	1.0E-78	11417304	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6743	16622		1.68	1.0E-78	U52373.1	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
9189	18924	25350	5.14	1.0E-78	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9284	18986	25327	1.26	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4600	14488	24274	4.48	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4758	14643	24431	2.48	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5335	15255	25078	12.03	9.0E-79	AB028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
5827	15733	25844	2.18	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
7243	17120	27315	4.99	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7243	17120	27316	4.99	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7953	17803	28042	1.31	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
7953	17803	28043	1.31	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
8419	18293	28547	1.82	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
8802	18616	28906	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
8802	18616	28907	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2), mRNA
9854	19347	25213	1.49	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3682	13596	23382	1.2	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4391	14287	24069	0.94	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4391	14287	24070	0.94	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
9107	15097	24889	1.4	8.0E-79	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
3214	13138	22941	6.85	7.0E-79	BE619648.1	EST_HUMAN	601472766T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
9040	18827		1.29	6.0E-79	AA699829.1	EST_HUMAN	zj94e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
8786	18601	28891	4.15	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3139	13064		1.12	4.0E-79	8922325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
4946	14823	24590	1.33	4.0E-79	BF210869.1	EST_HUMAN	601874522F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5'
310	10272	20091	1.4	3.0E-79	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
962	10885	20733	2.68	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cln) gene, complete cds
3060	12987	22778	1.36	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5291	15212	25012	4.52	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5506	15424	25486	1.71	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5525	15442	25507	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5525	15442	25508	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6200	15960	26091	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
6200	15960	26092	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
618	10555	20367	1.05	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
912	10836	20685	1.14	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1019	10937		1.43	2.0E-79	AI523747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
2101	11990	21888	14.14	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2101	11990	21889	14.14	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2146	12034	21931	0.99	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2265	12149	22049	1.54	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
3838	13749	23542	0.86	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
4074	13976	23755	1.17	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4590	14478	24265	0.96	2.0E-79	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
6251	16117	26270	1.83	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6251	16117	26271	1.83	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6956	16834	27029	2.6	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
7808	17658	27896	1.44	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
7808	17658	27897	1.44	2.0E-79	S72869.1	NT	H4(D10S170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8391	18267	28516	4.22	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
8391	18267	28517	4.22	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
9078	15096	24888	2.6	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
9161	18907	25341	4.23	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
9391	19050	25307	1.96	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
5971	19456		2.78	1.0E-79	BF363071.1	EST_HUMAN	MR0-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
8894	18704	28998	2.74	1.0E-79	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
3107	13033	22828	3.79	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3107	13033	22829	3.79	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
7751	17601	27824	1.28	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
8597	18464	28735	11.05	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
8597	18464	28736	11.05	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3551	13466		0.95	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
6485	16343	26512	2.83	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6485	16343	26513	2.83	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7409	17276	27482	1.19	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7409	17276	27483	1.19	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
882	10808	20657	2.34	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1624	11528	21386	2.05	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
4188	14088	23865	1.09	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4188	14088	23866	1.09	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5545	15461	25632	4.01	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
5702	15610	25712	2.56	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
5776	15683	25791	3.84	6.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7123	17000	27191	3.07	6.0E-80	11526484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
7123	17000	27192	3.07	6.0E-80	11526484	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
7214	17091	27281	1.74	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
7672	17522	27748	1.68	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
8311	18188	28437	2.91	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8555	18425	28694	50.71	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
9047	10808	20657	1.98	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
9172	19562		1.62	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9371	19037		4.55	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9847	19686		2.25	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
573	10511	20319	1.11	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
817	10745	20592	1.26	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
817	10745	20593	1.26	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1172	11084		4.77	5.0E-80	X91647.1	NT	H.sapiens ncx1 gene (exon 12)
1440	11345		2.28	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2311	12192	22091	0.92	5.0E-80	U89358.1	NT	Human l(3)mbt protein homolog mRNA, complete cds
2380	12260	22152	3.98	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2764	12626	22518	1.13	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
3953	13861	23636	1.07	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
3953	13861	23637	1.07	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4872	14752	24531	1.74	5.0E-80	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6866	16745	26938	1.48	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
7333	17237	27441	7.48	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
210	10181		4.71	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4610	14498	24287	1.43	3.0E-80	BF085009.1	EST_HUMAN	PM0-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4818	14701		4.97	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5554	15470	25541	2.05	3.0E-80	AI091675.1	EST_HUMAN	oo23e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:O35790 O35790 PIG-L. ;
1757	11656	21527	6.39	2.0E-80	R35321.1	EST_HUMAN	yg65a08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:38060 5'
1816	11713	21593	1.91	2.0E-80	AI444821.1	EST_HUMAN	RET4B7 subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2009	11901	21791	6.6	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D1323 5'
6132	15979	26115	1.58	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC90), mRNA
8243	18123	28373	3.06	2.0E-80	AA393362.1	EST_HUMAN	zt70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
337	10296		1.82	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
782	10712	20551	1.12	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1911	11806		3.13	1.0E-80	AI732656.1	EST_HUMAN	nn01f12.x5 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.t1 OFR repetitive element ;
4358	14264	24039	0.96	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5192	15055	24819	0.97	1.0E-80	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5265	15187		5.63	1.0E-80	BE386615.1	EST_HUMAN	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
5633	15547	25635	6.41	1.0E-80	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
5916	15822	25947	1.6	1.0E-80	5174540	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
6470	16329	26496	2.68	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
6470	16329	26497	2.68	1.0E-80	AI948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472296 3'
7350	17218	27417	1.23	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7350	17218	27418	1.23	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7957	17807	28049	1.19	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8044	17935	28183	7.42	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
8044	17935	28184	7.42	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
9443	19079	25281	1.45	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9643	19211	25258	1.86	1.0E-80	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
9670	19229		1.99	1.0E-80	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
8071	17962	28212	2.33	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
8071	17962	28213	2.33	8.0E-81	AI251752.1	EST_HUMAN	qh90g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
8494	18367	28631	4.95	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
6300	16164	26321	3.06	7.0E-81	AI822115.1	EST_HUMAN	za91c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299918 3'
4290	14188	23971	4.84	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4290	14188	23972	4.84	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5229	15153	24920	1.93	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5229	15153	24921	1.93	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7325	17201	27401	1.34	6.0E-81	AA360017.1	EST_HUMAN	EST69129 Fetal lung II Homo sapiens cDNA 5' end
9579	19166	25269	1.82	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
9679	19166	25270	1.82	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2170	12057	21960	3.14	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
6901	16780	26974	3.47	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6901	16780	26975	3.47	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8865	18677	28966	2.51	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11046), mRNA
214	10185	19998	0.87	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1779	11678	21556	0.99	4.0E-81	AW779612.1	EST_HUMAN	hn98d02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COPG_BOVIN P53620 COATOMER GAMMA SUBUNIT ;
3134	13059	22858	3.79	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3576	13490	23280	1.18	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815 STRIATIN. ;
4068	13970	23746	2.14	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4068	13970	23747	2.14	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6821	16700	26893	2.15	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(751) protein
6973	16850	27041	3.4	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6973	16850	27042	3.4	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
7320	17196	27396	5.65	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
7816	17666	27906	1.49	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
8522	18394	28658	2.24	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8522	18394	28659	2.24	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
9069	19627	25007	3.81	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9069	19627	25008	3.81	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9612	19191	25253	2.52	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
9612	19191	25254	2.52	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
9750	19275	25228	2.57	4.0E-81	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1246	11153	21000	9.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1246	11153	21001	9.36	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2320	12201	22100	1.7	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2961	12888	22685	5.12	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2961	12888	22686	5.12	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
4933	14811		0.87	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2802	12732	22530	1.77	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2802	12732	22531	1.77	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3707	13620	23404	0.98	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4579	14469	24256	0.85	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
9888	13620	23404	1.74	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
9898	19375	25194	1.35	2.0E-81	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1403	11308	21169	3.32	1.0E-81	W26539.1	EST_HUMAN	33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3602	13516	23304	2	1.0E-81	AW960658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
4414	14308	24091	3.07	1.0E-81	AA040370.1	EST_HUMAN	zk45h09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly ;
4546	14439	24222	7.85	1.0E-81	BE047996.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526 5'
5203	15083	29103	9.03	1.0E-81	U87928.1	NT	Human aconitate hydratase (ACO2) gene, exon 3
5284	15206	24982	4.01	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5284	15206	24983	4.01	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5468	15388	25449	3.54	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
5468	15388	25450	3.54	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
5737	15645	25750	3:15	1.0E-81	BF674641.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6567	16425	26606	6.4	1.0E-81	11432966	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7631	17482	27702	2.62	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
7631	17482	27703	2.62	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
7726	17576	27799	4.81	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
7819	17669	27909	2.93	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
7819	17669	27910	2.93	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
8000	17850	28091	1.46	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
8438	18312	28568	1.96	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
8438	18312	28569	1.96	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
8594	13516	23304	2.42	1.0E-81	AW960658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
8810	18624	28915	1.96	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
9278	18981	25325	3.62	1.0E-81	11418138	NT	Homo sapiens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
12	9998	19789	1.87	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
101	9998	19789	1.26	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
263	10228	20044	1.66	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
797	10726	20566	2.17	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
869	10795	20645	1.11	8.0E-82	U08988.1	NT	Human CRFB4 gene, partial cds
1475	11380	21244	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1636	11540	21400	1.24	8.0E-82	6715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4150	14050	23825	0.81	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1434	11339		1.27	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2739	12601	22495	1.82	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
4034	13937	23713	0.81	5.0E-82	AA515512.1	EST_HUMAN	nf69e11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925196 3'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1647	11551	21412	6.51	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
8954	18761	29054	6.47	4.0E-82	AI937300.1	EST_HUMAN	wp75e09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276 O75276 PKD1 ;
9519	19130		6.19	4.0E-82	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
276	10242	20061	13.75	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
687	10620	20446	2.19	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-f02 BN0120 Homo sapiens cDNA
770	10700	20539	4.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
852	10779	20629	3.22	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1046	10963		13.76	3.0E-82	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1333	11240	21098	5.47	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1450	11355	21219	2.03	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1859	11755	21630	1.82	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
1961	11855	21744	0.9	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3234	13158		2.06	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
4836	14718	24501	0.91	3.0E-82	AA135979.1	EST_HUMAN	zn93b04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE ;
6738	16617	26807	2.84	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
7654	17504	27728	3.79	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
7654	17504	27729	3.79	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
582	10520	20326	1.92	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
582	10520	20327	1.92	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1660	11562	21428	1.75	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3772	13684	23466	1.14	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4140	14040	23815	1.14	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4458	14352	24143	0.98	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4458	14352	24144	0.98	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4768	14653	24441	3.18	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5013	14887	24653	1.66	2.0E-82	4507680	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5013	14887	24654	1.66	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5358	15278	25108	2.37	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5746	15654	25762	4.96	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
6834	16713	26906	2.23	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
7821	17671	27912	1.2	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
7821	17671	27913	1.2	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
8628	18493	28766	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8628	18493	28767	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
9097	18868		2.23	2.0E-82	N94950.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
9632	19205		2.57	2.0E-82	AA011278.1	EST_HUMAN	zi01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
9923	19395		1.44	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
577	10515	20321	1.45	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1190	11100		0.9	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1264	11171	21020	1.91	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1265	11172	21021	0.83	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
7882	17732		1.38	1.0E-82	BF515938.1	EST_HUMAN	UI-H-BW1-aoa-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
8128	18016	28264	2.57	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8373	18250	28500	1.76	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7057	16934	27124	4.7	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
1392	11297	21165	1.88	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1656	12647	21422	1.96	8.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2836	12764		1.64	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4710	14596		5.49	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y3I6 Q9Y3I6 DJ207H1.1 ;
397	10343	20169	1.34	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1747	11647	21515	1.5	6.0E-83	AW573088.1	EST_HUMAN	hf31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN HI0034. ;
2984	12912	22709	1.09	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
3031	12959	22751	0.94	6.0E-83	AA701457.1	EST_HUMAN	zi59c05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435080 3'
3515	13431	23231	0.95	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5236	15160	24928	1.72	6.0E-83	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5669	15579	25679	2.13	6.0E-83	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
6430	16291	26452	1.79	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7579	17430	27644	6.77	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8817	18630		6.32	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR.t2 THR repetitive element ;
9050	18834		3.11	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
931	10856		4.14	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2004	12649		2.1	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3586	13500	23289	0.92	5.0E-83	AL133207.2	NT	Novel human gene mapping to chomosome X
5011	14885	24651	10.99	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5011	14885	24652	10.99	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5094	14964	24739	0.86	5.0E-83	AF083827.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11
624	10561	20373	1.47	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3469	13385	23190	0.96	4.0E-83	BE888078.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
981	10904		4.5	3.0E-83	AA368311.1	EST_HUMAN	EST79542 Placenta I Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2760	12612		1.82	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.t2 THR repetitive element ;
1759	11658	21529	1.9	2.0E-83	AA993492.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1759	11658	21530	1.9	2.0E-83	AA993492.1	EST_HUMAN	ot64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614 Q92614 MYELOBLAST KIAA0216. ;
1883	11779	21654	2.23	2.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
2821	12750	22542	1.11	2.0E-83	BE828694.1	EST_HUMAN	RC6-ET0046-280600-013-H12 ET0046 Homo sapiens cDNA
3231	13155		1.82	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3708	13621		1	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4241	14140	23915	4.47	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4553	14446	24230	8.13	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4553	14446	24231	8.13	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5359	15279	25109	23.35	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
5359	15279	25110	23.35	2.0E-83	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6396	16258	26419	5.9	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
6659	16539	26736	1.52	2.0E-83	U66707.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
6839	16718	26911	2.56	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
6839	16718	26912	2.56	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7767	17617	27845	3.32	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7767	17617	27846	3.32	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7826	17676	27920	1.21	2.0E-83	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
8223	18105	28358	3.7	2.0E-83	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8298	18177	28422	1.82	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5'
8298	18177	28423	1.82	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547J135 5'
9667	19226		3.48	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1390	11295	21152	16.57	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1390	11295	21153	16.57	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2620	12488	22378	1.6	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3146	13071	22872	0.84	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3793	13705	23491	3.55	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4151	14051	23826	2.22	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
4789	14674	24461	1.36	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6022	15926	26057	1.75	1.0E-83	AI027614.1	EST_HUMAN	ov99b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3727	13639	23425	2.82	7.0E-84	BE901209.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1273	11180	21028	4.21	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
1273	11180	21029	4.21	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2348	12228	22125	4.76	6.0E-84	AA776574.1	EST_HUMAN	ae86a03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5206	15085		6.24	6.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5388	15307	25160	1.7	6.0E-84	AA897339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
6415	16277	26440	3.17	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
6706	16586	26774	1.9	6.0E-84	BE770199.1	EST_HUMAN	PM4-FT0054-160600-004-e10 FT0054 Homo sapiens cDNA
8821	18634		1.94	6.0E-84	AW369812.1	EST_HUMAN	IL0-BT0168-091199-139-e06 BT0168 Homo sapiens cDNA
697	10630	20456	1.06	5.0E-84	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
2981	12908		1.01	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8830	18643	28926	2.76	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
1354	11260	21116	1.08	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1389	11294	21151	4.03	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR ;
4869	14749	24529	1.76	4.0E-84	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5060	14930	24701	1.27	4.0E-84	U94982.1	NT	Human 2,4-dienoyl-CoA reductase gene, exons 3 and 4
5416	15336	25388	1.31	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5416	15336	25389	1.31	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5791	15697	25805	2.35	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6507	16366	26543	12.16	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8290	18169	28413	6.56	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
313	10275	20094	1.36	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1137	11051	20891	0.89	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1917	11812	21690	1.15	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1962	11856	21745	3.03	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3542	13458	23251	1.18	3.0E-84	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3689	13602	23389	4.11	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds
8253	18133		7.8	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2058	11948	21845	5.89	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2058	11948	21846	5.89	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-b08 BT0795 Homo sapiens cDNA
2913	12840	22640	9.55	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-l) mRNA, complete cds
2932	12859	22659	0.93	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4682	14568	24364	1.11	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
4682	14568	24365	1.11	2.0E-84	BF308518.1	EST_HUMAN	601887664F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
6695	16575		1.67	2.0E-84	AI298674.1	EST_HUMAN	qm87c09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
9308	19003	25334	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
9308	19003	25335	1.89	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
309	10271	20090	1.53	1.0E-84	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
537	10478	20290	5.2	1.0E-84	4507952	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
703	10636		0.99	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1271	11178	21026	1.92	1.0E-84	AA984379.1	EST_HUMAN	am85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2008	11900	21790	3.13	1.0E-84	BE392137.1	EST_HUMAN	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2176	12063	21964	1.08	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3691	13605	23391	2.14	1.0E-84	AA720851.1	EST_HUMAN	nw12e06.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4319	14216	23998	5.59	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4601	14489	24275	3.82	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4601	14489	24276	3.82	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4823	14216	23998	4.29	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5757	15665	25773	1.52	1.0E-84	S73482.1	NT	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6113	16007	26143	1.49	1.0E-84	AL049784.1	NT	Novel human gene mapping to chomosome 13
6113	16007	26144	1.49	1.0E-84	AL049784.1	NT	Novel human gene mapping to chomosome 13
6220	16086	26236	1.96	1.0E-84	AL049784.1	NT	Novel human gene mapping to chomosome 13
6414	16276	26439	3.12	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6483	16324	26490	1.8	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7495	17365		2.45	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
7639	15091	24884	1.85	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7639	15091	24885	1.85	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9190	18925		2.98	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
9298	18998	25330	9.8	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
951	10875		1.17	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1057	10974	20816	2.3	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1057	10974	20817	2.3	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1560	11465	21322	1.07	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1560	11465	21323	1.07	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1651	11554	21417	4.93	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4158	14058	23832	0.94	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4778	14662	24449	1.14	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4825	14707	24491	1.01	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
9819	11554	21417	1.27	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1120	11035	20877	3.24	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8910	18718		5.81	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
8718	18535	28819	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8718	18535	28820	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2285	12168	22066	1.21	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8462	18335	28598	1.9	6.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9886	15094		2.45	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
5738	15646	25751	1.66	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
5738	15646	25752	1.66	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
8017	17867		1.68	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
9237	19549		1.97	4.0E-85	Z18867.1	EST_HUMAN	HSDHEGC03 Stratagene cDNA library Human heart, cat#936208 Homo sapiens cDNA clone HEGC03
1277	11185	21035	1.15	3.0E-85	AF096157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1741	11642	21509	3.37	3.0E-85	T97495.1	EST_HUMAN	ye53g09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4219	14117	23894	0.94	3.0E-85	BE267189.1	EST_HUMAN	601189704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4805	14689	24475	1.73	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4805	14689	24476	1.73	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4864	14744	24523	8.66	3.0E-85	AB046783.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
4883	14764	24540	0.94	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5729	15636	25739	6.94	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
5729	15636	25740	6.94	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6152	16025		7.04	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6594	16474	26663	1.61	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
7190	17067	27256	4.06	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
8796	18610	28901	2.28	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
9788	19298		2.66	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
947	10871	20719	0.87	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1024	10942	20786	1.85	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1400	11305	21164	7.1	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1400	11305	21165	7.1	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2183	12070	21972	2.12	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2793	11222		4.24	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
4239	14138	23913	5.42	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4822	14705	24489	1.3	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7341	17209	27408	1.29	2.0E-85	AI760820.1	EST_HUMAN	wi67h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element ;
2241	12125		2.44	1.0E-85	BE794306.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2344	12224	22121	8.09	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2344	12224	22122	8.09	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7632	17483	27704	2.06	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
8296	18175	28419	2.56	1.0E-85	AA778785.1	EST_HUMAN	zj45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
8296	18175	28420	2.56	1.0E-85	AA778785.1	EST_HUMAN	zj45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
8365	18242	28492	2.28	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
8365	18242	28493	2.28	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
9194	19082	25283	2.7	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9448	19082	25283	3.43	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1410	11316		7.66	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
220	10190	20001	1.3	7.0E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
921	10845	20691	1.33	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
921	10845	20692	1.33	7.0E-86	AA860801.1	EST_HUMAN	aj88f08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6164	15121	24865	6.91	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
7078	16955	27148	2.91	7.0E-86	L38557.1	NT	Homo sapiens galactocerebrosidase (GALC) gene, exon 15
7593	17444		1.63	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
7624	17475	27696	2.35	7.0E-86	11526307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
8329	18206	28455	2.15	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
8329	18206	28456	2.15	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
1272	11179	21027	9.33	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH) mRNA
204	10175	19993	1.48	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5677	15586	25686	10.18	4.0E-86	BE295843.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
8567	10175	19993	1.9	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5435	15355	25411	6.02	3.0E-86	AW340946.1	EST_HUMAN	xz92h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
7868	17718	27963	3.31	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7868	17718	27964	3.31	3.0E-86	BE886479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
8734	17883	28125	9.01	3.0E-86	AI659240.1	EST_HUMAN	tu18b02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251371 3'
9163	19560		2.02	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
266	10231	20046	1.33	2.0E-86	AA306264.1	EST_HUMAN	EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
408	10354		1.67	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1173	11085	20929	2.18	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:283478 5'
2144	12032	21930	2.37	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
2222	12107	22011	1.12	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3369	13288	23087	1.43	2.0E-86	AW966142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3686	13599	23385	2.16	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3686	13599	23386	2.16	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3954	13862		2.42	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'
4679	14565	24360	2.8	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5580	15495	25571	1.53	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5580	15495	25572	1.53	2.0E-86	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
6987	16864	27057	2.22	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6987	16864	27058	2.22	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
7372	17241	27446	1.95	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
7969	17819	28061	2.69	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7969	17819	28062	2.69	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
8276	18156	28397	1.83	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
9606	19187	25250	2.4	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9772	19290		1.81	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9955	19520	25139	1.47	2.0E-86	11417883	NT	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA
1579	11483	21343	3.1	1.0E-86	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3125	13050	22847	2.06	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3197	13122	22927	2.42	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3256	13179	22977	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3256	13179	22978	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3864	13775	23568	11.48	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3864	13775	23569	11.48	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4167	14067	23842	5.76	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4832	14714	24497	1.11	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKB23 isoform mRNA, complete cds
8882	15328	25378	2.15	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5287	15209		1.47	9.0E-87	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6403	16264	26424	2	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6403	16264	26425	2	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
471	10414	20233	14.17	8.0E-87	X62245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2250	12134	22031	2.74	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2250	12134	22032	2.74	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6763	16642	26829	2.67	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA
7794	17644	27877	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
7794	17644	27878	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8264	18144	28384	10.88	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
8264	18144	28385	10.88	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3482	13398	23203	0.87	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5868	15774	25893	1.73	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
8107	17997		3.52	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1142	11056	20898	1.69	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
9450	11056	20898	1.53	5.0E-87	AA382811.1	EST_HUMAN	EST96094 Testis I Homo sapiens cDNA 5' end
950	10874	20721	1.33	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1155	11068	20912	10.54	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1411	11316	21179	0.86	4.0E-87	R78133.1	EST_HUMAN	yi80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
1985	11878	21771	0.92	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2372	12252	22142	1.07	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2372	12252	22143	1.07	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3419	13336	23140	2.19	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5343	15264	25090	6.47	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5686	15595	25696	4.36	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
8505	18378	28644	4.35	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8994	18798	29091	2.13	4.0E-87	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
9695	19246		14.77	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2749	12611	22502	2.99	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3717	13629	23414	0.89	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4826	14708	24492	1.17	2.0E-87	BF376311.1	EST_HUMAN	CM0-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4880	14760	24537	0.8	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
5473	15393	25457	7.87	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5473	15393	25458	7.87	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5819	15726		6.27	2.0E-87	BE567193.1	EST_HUMAN	601341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6256	16122	26275	1.51	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
6407	16268	26430	32.21	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6526	16385	26564	28.31	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6892	16771	26966	3.81	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
7634	17485		5.11	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1165	12645		2.33	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1413	11318	21181	0.94	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1413	11318	21182	0.94	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3649	13563	23349	3.18	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3673	13587	23374	2.47	1.0E-87	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
5057	14927	24699	1.04	1.0E-87	U50949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
5774	15681	25788	3.39	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
5774	16681	25789	3.39	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6376	16238	26398	1.6	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6724	16604	26793	13.13	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
7165	17042	27233	1.19	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
7165	17042	27234	1.19	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
7554	17405	27620	2.77	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
7554	17405	27621	2.77	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
8114	18003	28249	2.06	1.0E-87	5729867	NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA
8367	18244		1.78	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
9639	19751		2.02	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1090	11006	20847	7.39	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	11234	21090	2	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1327	11234	21091	2	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3574	13488	23279	1.13	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4172	14072	23847	2.64	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4172	14072	23848	2.64	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4934	14812	24580	1.23	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7216	17093	27284	3.69	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1787	11685		1.19	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2602	12470	22366	3	5.0E-88	N89399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2970	12897	22696	0.92	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2978	12905	22704	0.94	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2978	12905	22705	0.94	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3343	13263		2.31	5.0E-88	AI693217.1	EST_HUMAN	wd68h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element;contains element MER22 MER22 repetitive element ;
3491	13407	23212	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
4631	14519	24310	0.87	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6059	16042	26185	2.64	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5'
6627	16507	26694	1.84	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1307	11214	21070	1.64	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1307	11214	21071	1.64	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
6295	16159	26316	1.93	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
8281	18160	28402	2.84	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
8780	18595	28883	2.1	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8780	18595	28884	2.1	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
715	10647	20475	0.93	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1770	11669		4.77	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2918	12845	22647	4.31	3.0E-88	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4147	14047	23819	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4147	14047	23820	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4380	14276		3.17	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5242	15166	24937	4.09	3.0E-88	11429567	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5429	15349	25403	3.84	3.0E-88	9966888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5498	15417	25480	3.39	3.0E-88	11420697	NT	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6204	15964	26098	12.03	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6452	16313	26479	6.66	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
6620	16500	26688	8.52	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6769	16648	26836	1.41	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds
7427	16440	26626	2.12	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9286	18988		4.78	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1020	10938	20780	1.42	2.0E-88	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1607	11512	21372	0.93	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1716	11617	21486	4.19	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4328	14225	24007	1.93	2.0E-88	5031666	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
5604	15518	25597	4.98	1.0E-88	AW139565.1	EST_HUMAN	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5604	15518	25598	4.98	1.0E-88	AW139565.1	EST_HUMAN	UI-H-BI1-aea-d-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6004	15909	26033	17.59	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6004	15909	26034	17.59	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6263	16128	26282	4.06	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851 ;
7524	17375	27584	2.95	1.0E-88	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
8742	17891	28135	2.27	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
9502	19117		2.98	1.0E-88	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8321	18198	28447	4.12	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
2705	12568	22459	1.41	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
426	10371	20194	1.35	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
426	10371	20195	1.35	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4785	14670	24457	2.94	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4847	14728	24511	5.14	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
5334	15254	25076	1.35	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
5334	15254	25077	1.35	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
6428	16289	26450	1.78	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
8006	17856	28097	1.42	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
8006	17856	28098	1.42	7.0E-89	X62048.1	NT	H.sapiens Wee1 hu gene
8012	17862	28107	1.17	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8012	17862	28108	1.17	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9920	19393		3.07	7.0E-89	U87927.1	NT	Human aconitate hydratase (ACO2) gene, exon 2
1006	10924	20768	1.07	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
2166	12063	21954	1.12	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2383	12263	22154	1.97	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2383	12263	22155	1.97	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3480	13396	23201	0.84	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4537	14430	24211	3.5	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4537	14430	24212	3.5	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5007	14881	24646	2.77	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5007	14881	24647	2.77	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
6477	16336	26503	1.33	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA
2847	12775	22563	1.61	3.0E-89	AW976181.1	EST_HUMAN	EST388290 MAGE resequences, MAGN Homo sapiens cDNA
9688	19241	25215	1.92	3.0E-89	AV705749.1	EST_HUMAN	AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'
121	10348	20175	1.46	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
121	10348	20176	1.46	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	10348	20175	0.91	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
402	10348	20176	0.91	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
519	10461	20272	0.83	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2852	12780	22569	2.01	2.0E-89	AI222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPEPTIDASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
4053	13955	23731	1.45	2.0E-89	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4061	13963	23740	6.18	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4061	13963	23741	6.18	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4396	14292	24076	1.14	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5368	15288	25123	2.5	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
5538	15455	25525	1.6	2.0E-89	U03985.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6520	16379	26557	4.93	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
6630	16510	26699	3.73	2.0E-89	11428801	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8680	18568	28851	2.63	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
8854	18666	28953	4.87	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
8955	18762	29055	2.24	2.0E-89	U10692.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8860	18672	28960	6.12	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
8860	18672	28961	6.12	1.0E-89	BF196052.1	EST_HUMAN	hr81d09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
6789	16668	26859	1.16	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6789	16668	26860	1.16	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1047	10965	20806	1.62	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1048	10965	20806	2.93	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1308	12690	21072	5.28	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1308	12690	21073	5.28	8.0E-90	BE670561.1	EST_HUMAN	7e36f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
818	10746		2.65	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6907	16785		1.91	7.0E-90	AA782977.1	EST_HUMAN	ai63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
7183	17060	27250	1.88	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
7183	17060	27251	1.88	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
7833	17683	27927	1.98	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
7833	17683	27928	1.98	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
3029	12957	22749	1.14	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
3029	12957	22750	1.14	6.0E-90	X91926.1	NT	H.sapiens ECE-1 gene (exon 6)
4134	14034	23809	7.33	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4134	14034	23810	7.33	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5641	15554	25646	3.54	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
5641	15554	25647	3.54	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6846	16725	26918	3.25	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
6846	16725	26919	3.25	6.0E-90	4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
149	10123		10.5	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 1-10b
1175	11087	20931	1.55	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
2508	12382	22273	2.19	5.0E-90	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4440	14334	24124	3.08	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4507	14400	24186	1.07	5.0E-90	AA705222.1	EST_HUMAN	zj82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4507	14400	24187	1.07	5.0E-90	AA705222.1	EST_HUMAN	zj82g10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:461442 3'
4571	14463	24251	0.98	5.0E-90	AL135549.1	EST_HUMAN	DKFZp762P1616_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762P1616 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5433	15353	25409	2.52	5.0E-90	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5523	15353	25409	2.13	5.0E-90	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
6283	16147	26302	2.26	5.0E-90	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
6283	16147	26303	2.26	5.0E-90	AF113708.1	NT	Homo sapiens angiopoietin 4 (ANG4) mRNA, partial cds
6464	16323	26489	7.93	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
6825	16704	26899	4.66	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7581	17432	27646	1.24	5.0E-90	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7968	17818	28060	15.41	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9744	19306		2.16	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9789	19299		2.37	5.0E-90	AI523366.1	EST_HUMAN	ar78h05.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
299	10263	20083	1.85	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
299	10263	20084	1.85	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1070	10986	20829	2.94	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1663	11565	21432	9.22	4.0E-90	X99033.1	NT	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
4567	14449	24235	4.07	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4691	14577	24372	1.97	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4713	14599	24385	1.9	4.0E-90	M95967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
8901	18709	29004	103.62	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
207	10178	19995	4.28	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1156	11069	20913	3.65	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1156	11069	20914	3.65	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3771	13683	23465	2.81	2.0E-90	AI138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1713410 3' similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
4588	14476	24264	1.13	2.0E-90	AB006627.1	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
4820	14703	24488	8.33	2.0E-90	5729855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5534	15451	25519	4.34	2.0E-90	AW672686.1	EST_HUMAN	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN. ;
7638	17489	27708	2.9	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
7638	17489	27709	2.9	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
7722	17572	27796	1.56	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7722	17572	27797	1.56	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
8765	17914	28159	49.27	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
275	10241	20060	3.39	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
370	12639	20148	1.21	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
371	12639	20148	1.04	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
680	10613	20435	2.03	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
680	10613	20436	2.03	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	10645	20472	7.71	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	10645	20473	7.71	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1094	11010		2.45	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1284	11192	21044	3.47	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1284	11192	21045	3.47	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1644	11648		4.02	1.0E-90	BE379884.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1860	11756	21631	4.98	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2823	12752	22645	8.4	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3777	13689	23473	1.18	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3777	13689	23474	1.18	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4326	14223	24005	1	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5481	15401	25464	2.2	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6521	16380	26558	2.85	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
7121	16998	27189	3.78	1.0E-90	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
7356	17224		1.22	1.0E-90	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7371	17240	27444	1.72	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
7371	17240	27445	1.72	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9732	19268	25225	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
9732	19268	25226	1.89	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4101	14001	23780	5.48	8.0E-91	D12234.1	EST_HUMAN	HUM000S381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
1428	11333	21199	0.88	7.0E-91	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
6835	16714	26907	2.05	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
3429	13346	23151	1.47	5.0E-91	AA702794.1	EST_HUMAN	zi90b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4415	14309	24092	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4415	14309	24093	1.05	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4703	14589	24379	0.82	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4703	14589	24380	0.82	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
7087	16964	27157	1.34	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
7087	16964	27158	1.34	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
3166	13091	22895	1.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3166	13091	22896	1.3	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
8301	18180	28427	3.13	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9239	18954	25314	1.67	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
9239	18954	25360	1.67	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1601	11506	21366	5.12	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1601	11506	21367	5.12	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2624	12492	22382	0.99	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
2624	12492	22383	0.99	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
3297	13219	23020	1.77	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3416	13333	23136	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3416	13333	23137	2.96	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3720	13632	23418	0.83	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4487	14381	24168	4.02	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4905	14785	24560	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4905	14785	24561	1.2	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5488	15407	25470	1.45	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
5807	15712		2.39	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
5967	15872	25996	4.11	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
5967	15872	25997	4.11	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6502	16361	26535	4.4	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
6502	16361	26536	4.4	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7093	16970	27163	3.31	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9480	19104	25286	1.45	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9812	12492	22382	3.03	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
9812	12492	22383	3.03	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
42	10030	19833	3.02	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1225	11133	20987	3.58	1.0E-91	AW449746.1	EST_HUMAN	UI-H-BI3-aks-d-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
6090	16035	26175	1.7	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6090	16035	26176	1.7	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
9398	19685		2.42	1.0E-91	H15212.1	EST_HUMAN	ym30e03.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:49587 5'
1221	11130	20981	8.41	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
1221	11130	20982	8.41	9.0E-92	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
5353	15273	25103	3.56	9.0E-92	J03007.1	NT	Human Na+,K+ ATPase alpha-subunit mRNA, partial cds
5442	15362	25418	1.75	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
5882	15789	25911	3.22	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6878	16757	26954	19.33	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
6878	16757	26955	19.33	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
7342	17210	27409	1.66	9.0E-92	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
87	10071	19887	2.02	8.0E-92	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
283	10248	20068	5.9	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1778	11677	21554	1.29	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
1778	11677	21555	1.29	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
5944	15849	25973	1.29	8.0E-92	AJ000979.1	NT	Homo sapiens MCP-4 gene
6908	16786	26978	3.61	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
6908	16786	26979	3.61	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
7242	17119	27314	2.61	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
7760	17610	27836	1.31	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
8180	18067	28316	4.53	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
8667	18556	28841	3.21	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
9572	19162	25268	1.43	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
60	10046	19858	2.64	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
236	12662	20020	2.51	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
236	12662	20021	2.51	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
676	10514		1.25	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1259	11166	21017	1.91	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2139	12027	21923	1.67	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2139	12027	21924	1.67	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2517	12391	22283	2.32	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2693	12558	22445	5.01	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2724	12586	22481	1.04	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3301	15068	23023	0.92	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3301	15068	23024	0.92	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4484	14378	24165	1.61	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4484	14378	24166	1.61	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5110	14978	24762	1.45	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5219	15142	24836	4.87	7.0E-92	AA446206.1	EST_HUMAN	zw66d12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
1569	11473		0.93	6.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2738	12600	22494	2.45	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902939 5'
5583	15498	25575	3.74	3.0E-92	AA378336.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to ribosomal protein S13
8146	18034	28281	5.7	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
8146	18034	28282	5.7	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
23	10010	19803	1.53	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
172	10143	19958	2.93	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
172	10143	19959	2.93	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462O23.2 (DJ462O23.2), mRNA
732	10664	20497	1.38	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
732	10664	20498	1.38	2.0E-92	BE299190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1686	11588		2.74	2.0E-92	S78653.1	NT	mrg=mas-related [human, Genomic, 2416 nt]
1894	11789	21667	1.55	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
1894	11789	21668	1.55	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2002	11895	21787	4.71	2.0E-92	4506860	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
2623	12491	22381	37.64	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3562	13476	23265	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3562	13476	23266	1.02	2.0E-92	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3631	13545	23332	4.99	2.0E-92	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4191	14091	23869	1.02	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4648	14534	24323	0.79	2.0E-92	AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
4922	14801		2.53	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0414 5'
5989	15894	26017	2.49	2.0E-92	AB028991.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
6420	16273		2.25	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7141	17018	27211	1.37	2.0E-92	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
8142	18030	28276	5.91	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
9589	19172	25274	2.55	2.0E-92	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9839	12491	22381	26.65	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1807	11704	21582	1.11	1.0E-92	R78078.1	EST_HUMAN	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1807	11704	21583	1.11	1.0E-92	R78078.1	EST_HUMAN	yi80e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2028	11919	21810	34.72	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
7286	17162	27360	4.04	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
7286	17162	27361	4.04	1.0E-92	AI380356.1	EST_HUMAN	tg01b02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element ;
1983	11876	21769	3.14	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
1996	11890		9.21	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2610	12478		1.46	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3563	13477	23267	0.96	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
8911	18719		9.8	9.0E-93	11418526	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
5975	15879	26003	2.49	8.0E-93	BF036364.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
246	10212	20028	6.24	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1359	11265	21121	1.25	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1385	11290	21145	5.39	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1385	11290	21146	5.39	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314670 3'
1459	11364		0.95	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3195	13120	22925	2.42	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6540	16398	26577	3.67	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
7549	17400	27613	2.07	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7644	17494	27715	1.31	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
8200	18085	28336	3.01	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
9487	19423	25173	1.84	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
82	10066		4.72	4.0E-93	AA459933.1	EST_HUMAN	zx50e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM ;
437	10381	20204	1.75	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
437	10381	20205	1.75	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
755	10685	20522	1.33	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
755	10685	20523	1.33	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1166	11078	20923	2.08	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1934	11829	21712	5.06	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2349	12229	22126	0.84	4.0E-93	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2564	12435	22328	2.18	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3962	13869	23647	1.44	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5465	15385	25445	4.81	4.0E-93	T46864.1	EST_HUMAN	yb94c12.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ;
8475	18348	28613	19.24	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKCDRF07 5'
3601	13515	23302	5.99	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3601	13515	23303	5.99	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4142	14042		2.7	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
5535	15452	25520	1.58	3.0E-93	AI553853.1	EST_HUMAN	tn29g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
5535	15452	25521	1.58	3.0E-93	AI553853.1	EST_HUMAN	tn29g03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169076 3'
5952	15857	25979	1.32	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
8178	18066	28314	4.16	3.0E-93	AI824829.1	EST_HUMAN	wb02d05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
183	10155	19970	8.31	2.0E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
183	10155	19971	8.31	2.0E-93	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
320	10282	20100	6.69	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
321	10282	20100	7.68	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1598	11503	21363	1.48	2.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
2083	11973	21868	1.02	2.0E-93	U40763.1	NT	Human Clk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2436	12313	22210	0.89	2.0E-93	BE252982.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5088	14958	24732	1.02	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5325	15245	25049	4.59	2.0E-93	AW964385.1	EST_HUMAN	EST376458 MAGE resequences, MAGH Homo sapiens cDNA
5462	15382	25442	1.52	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
6014	15918		1.32	2.0E-93	AW502002.1	EST_HUMAN	UI-HF-BN0-aks-g-09-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
8996	19476	29093	2.87	2.0E-93	AI312025.1	EST_HUMAN	qp78b10.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1929115 3'
9386	19046		1.52	2.0E-93	AA126735.1	EST_HUMAN	zl29c10.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503346 3'
9465	19095		1.31	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
9724	19263		2.75	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
96	10081	19897	1.64	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
96	10081	19898	1.64	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
607	10449	20262	2.56	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
585	10523	20330	3.75	1.0E-93	AI146755.1	EST_HUMAN	oy84b08.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384 ZINC FINGER PROTEIN. ;
864	10781	20631	3.32	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	11125	20974	6.41	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1217	11125	20975	6.41	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1321	11228	21083	1.55	1.0E-93	AB046783.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
1323	11230	21085	1.68	1.0E-93	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2289	12172	22070	1.01	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2415	12292	22190	4.16	1.0E-93	AF055066.1	NT	Homo sapiens MHC class 1 region
2459	12336		1.09	1.0E-93	AL137200.1	NT	Novel human gene mapping to chomosome 1
2792	11181	21030	2.69	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2792	11181	21031	2.69	1.0E-93	BE297369.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2903	12830	22627	4.33	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4331	14228	24010	1.44	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5417	15338	25391	1.62	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5417	15338	25392	1.62	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5607	15522	25604	9.15	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6067	16051	26197	2.06	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6299	16163	26320	4.09	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
6807	16686	26876	2.04	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6971	16848	27039	1.18	1.0E-93	Y10183.1	NT	H.sapiens mRNA for MEMD protein
7024	16901	27093	1.59	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
7437	16450	26640	1.8	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7440	16453	26643	1.22	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
7529	17380	27589	4.54	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
7529	17380	27590	4.54	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9051	19494	25132	5.92	1.0E-93	AI268262.1	EST_HUMAN	qm03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:T19B4.4 CE13742 ;
9716	19257		2.33	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8025	17875		1.22	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3880	13791	23579	1.74	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
9830	19331		1.67	6.0E-94	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5296	15217	25019	3.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5296	15217	25020	3.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
5689	15598	25699	1.72	5.0E-94	AA722434.1	EST_HUMAN	zg87g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'
6183	16069	26218	1.63	5.0E-94	AI015800.1	EST_HUMAN	ot83d05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
9361	19736	24911	4.68	5.0E-94	T89398.1	EST_HUMAN	yd98b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'
9901	19378		1.27	5.0E-94	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
9907	19384		1.26	5.0E-94	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
1799	11697		4.55	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2621	12489	22379	0.86	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4618	14506	24295	3.02	4.0E-94	AI591312.1	EST_HUMAN	tw11f10.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
5892	15798	25921	1.84	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
5892	15798	25922	1.84	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8749	17898	28142	1.72	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
595	10531	20339	1.17	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
704	10637	20462	1.17	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1706	11607	21477	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1706	11607	21478	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1735	11636	21504	3.45	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4095	13995	23772	0.82	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:774782 5'
5484	15403	25466	3.58	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
5881	15787	25909	4.16	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6771	16650	26838	1.16	3.0E-94	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
6992	16869	27062	3.79	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
7533	17384	27596	4.36	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
8448	18321	28580	1.75	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
8928	18736	29029	2.27	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
143	10117	19937	2.24	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3050	12977	22769	1.91	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3050	12977	22770	1.91	1.0E-94	BE253433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4261	14160	23938	1.13	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
7331	17235	27439	1.93	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
7636	17487	27707	1.41	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
8418	18292	28546	2.49	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
8635	18500	28775	2.19	1.0E-94	AI272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845 Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR. ;
9769	10117	19937	1.98	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1461	11366	21230	1.55	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3118	13043	22839	1.13	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3118	13043	22840	1.13	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6801	16680	26869	1.87	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4436	14331	24119	1.59	8.0E-95	AI700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
4436	14331	24120	1.59	8.0E-95	AI700998.1	EST_HUMAN	we09e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
6294	16158	26314	1.83	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6294	16158	26315	1.83	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6770	16649	26837	2.05	8.0E-95	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
7391	17309	27515	1.73	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7391	17309	27516	1.73	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7667	17517	27744	2.82	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7681	17531		2.83	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8096	17987	28236	2.41	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
9689	19242		8.68	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.t1 L1 repetitive element ;
274	10240	20058	9.46	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
274	10240	20059	9.46	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4270	14169	23947	5.94	7.0E-95	M95708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4316	14213		1.38	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4982	14857	24623	1.03	7.0E-95	M95929.1	NT	Human homeobox protein (PHOX1) mRNA, 3' end
5340	15261	25087	1.76	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
922	10847	20694	0.86	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1625	11529	21387	1.6	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1625	11529	21388	1.6	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1897	11793	21672	7.79	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1900	11796	21676	3.3	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2376	12256	22147	1.3	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2376	12256	22148	1.3	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2417	12294	22191	16.55	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2466	12342	22236	2.46	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2787	10846	20693	0.86	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3120	13045	22842	3.51	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3517	13433	23232	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3517	13433	23233	2.78	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3565	13479	23268	0.96	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3690	13604	23390	1.02	2.0E-95	AI290264.1	EST_HUMAN	qm01c02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705 ;
4264	14163	23940	2.3	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
4971	14846	24615	2.57	2.0E-95	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5022	14895	24663	0.98	2.0E-95	AA447931.1	EST_HUMAN	zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5022	14895	24664	0.98	2.0E-95	AA447931.1	EST_HUMAN	zx11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5367	15287	25121	3.69	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5367	15287	25122	3.69	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5734	15642	25748	4.54	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
5957	15862	25984	2.25	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6055	16038	26179	1.62	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
8106	17996	28245	2.36	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPR1A) mRNA
9452	19084	25285	1.98	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9840	19338	25211	4.34	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5450	15371	25427	7.73	1.0E-95	AA284651.1	EST_HUMAN	zt23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
5460	15371	25428	7.73	1.0E-95	AA284651.1	EST_HUMAN	zt23h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
6437	16298	26460	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6437	16298	26461	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6767	16646	26835	1.67	9.0E-96	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
435	12666	20201	0.82	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
436	12666	20202	0.82	8.0E-96	BE907607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5383	15302		2.66	8.0E-96	AW836047.1	EST_HUMAN	PM0-LT0019-090300-002-d09 LT0019 Homo sapiens cDNA
3834	13746	23538	0.95	7.0E-96	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
2213	12099	22003	0.85	6.0E-96	BE171984.1	EST_HUMAN	MR0-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
3276	13197	22997	0.96	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3437	13354	23159	26.15	6.0E-96	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end
8831	18644	28927	1.98	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8831	18644	28928	1.98	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8870	18682	28972	2.09	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
317	10279	20096	2.7	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	10751	20599	3.06	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	10751	20600	3.06	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2576	12447		2.31	5.0E-96	11416767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2991	12919	22713	0.98	5.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
4810	14694		1.22	5.0E-96	X60812.1	NT	H.sapiens DNA for monoamine oxidase type A (7) (partial)
6065	16048	26193	4.23	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6065	16048	26194	4.23	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6719	16599	26788	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
6719	16599	26789	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4097	13997		6.22	3.0E-96	H68656.1	EST_HUMAN	yr87h12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212327 5'
409	10355		3.49	2.0E-96	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
730	10662	20494	1.56	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4651	14537	24326	1.58	2.0E-96	BE148074.1	EST_HUMAN	RC3-HT0230-040500-110-g02 HT0230 Homo sapiens cDNA
7191	17068		5.08	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCFMD07 5'
9151	18902		2.05	2.0E-96	AW249440.1	EST_HUMAN	2819351.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819351 5'
655	10590	20408	1.69	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1742	11643	21510	2.03	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1742	11643	21511	2.03	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGC Homo sapiens cDNA
1806	11703	21580	0.89	1.0E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
1806	11703	21581	0.89	1.0E-96	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2181	12068	21969	1.33	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2181	12068	21970	1.33	1.0E-96	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
2219	12650	22009	1.88	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
7058	16935	27125	20.65	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7138	17015	27208	1.98	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7843	17693	27938	1.64	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
7843	17693	27939	1.64	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
3285	13206	23006	0.95	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
6459	16319		2.75	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011099-004-D07 HT0117 Homo sapiens cDNA
6672	16552	26747	1.76	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
6735	16614	26804	10.79	5.0E-97	AA418026.1	EST_HUMAN	zv97e12.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125 G1304125 PMS4 MRNA ;
7578	17429	27643	2.76	5.0E-97	BF154912.1	EST_HUMAN	RC0-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
8832	18645	28929	1.87	5.0E-97	BE148597.1	EST_HUMAN	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
8832	18645	28930	1.87	5.0E-97	BE148597.1	EST_HUMAN	MR0-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
924	10849	20697	1.26	4.0E-97	BE004436.1	EST_HUMAN	CM0-BN0106-170300-293-a06 BN0106 Homo sapiens cDNA
1868	11764	21638	1.08	4.0E-97	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6082	16027	26167	6.1	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6082	16027	26168	6.1	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6867	16746	26939	1.41	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
7328	17232	27433	1.17	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds

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Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7328	17232	27434	1.17	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
8503	18376	28641	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8503	18376	28642	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8733	17882	28124	15.68	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
8736	17885	28128	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
8736	17885	28129	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1290 protein, partial cds
9331	19012		3.83	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
243	10210	20026	1.17	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
856	10783	20633	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
856	10783	20634	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1423	12694	21195	1.77	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2389	12652	22161	1.92	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3223	13147	22948	1.14	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
4670	14556	24349	12.55	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
5872	15778	25897	2.19	1.0E-97	BE566486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
8088	17979	28229	3.41	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8088	17979	28230	3.41	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8629	18494	28768	2.82	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3'
8763	17912	28156	13.54	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
8763	17912	28157	13.54	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
883	10809	20658	8	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1255	11162	21012	1.29	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6623	16503	26691	4.74	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
6623	16503	26692	4.74	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7271	17148	27342	2.77	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
7319	17195	27395	2.41	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
7355	17223	27423	1.39	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
8369	18246	28497	2.24	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8369	18246	28498	2.24	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
9345	10809	20658	4.97	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1350	11256	21112	0.89	8.0E-98	AB033768.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1540	11444	21303	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1540	11444	21304	1.04	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1695	11597	21468	0.98	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1695	11597	21469	0.98	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3726	13638	23424	5.03	8.0E-98	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5049	14921		0.88	8.0E-98	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
9717	19258	25220	1.29	4.0E-98	BE348727.1	EST_HUMAN	ht68f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3'
2131	12019	21917	1.21	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
2565	12436	22329	1.85	3.0E-98	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2720	12582		2.09	3.0E-98	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6147	16020	26159	1.7	3.0E-98	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6147	16020	26160	1.7	3.0E-98	. 11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7083	16960	27153	3.31	3.0E-98	H46698.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
7685	17535	27759	1.6	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
7685	17535	27760	1.6	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone I8
8322	18199	28448	5.15	3.0E-98	U59309.1	NT	Human fumarase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9895	19373		2.47	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
2033	11924	21816	29.05	2.0E-98	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2191	12078	21983	1.45	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4199	14099	23880	0.96	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4244	14143	23916	4.94	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4720	14606	24390	1.51	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
4720	14606	24391	1.51	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRN) gene, exon 16
5069	14939	24711	6.39	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA
5069	14939	24712	6.39	2.0E-98	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA
5163	15029	24795	1.09	2.0E-98	4758975	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
5303	15224	25028	4.66	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor I (LOC51735), mRNA
7004	16881	27073	3.87	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7004	16881	27074	3.87	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7497	17367	27572	1.5	2.0E-98	X12664.1	NT	H.sapiens arginase gene exon 3 (EC 3.5.3.1)
7951	17801		1.18	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
9350	19026	25301	1.43	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
399	10345	20172	18.93	1.0E-98	AI862007.1	EST_HUMAN	tw36b04.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
447	10391	20212	2.38	1.0E-98	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
1756	11655	21526	16.96	1.0E-98	N49818.1	EST_HUMAN	yv23f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5256	15178	24953	6.96	1.0E-98	AA195854.1	EST_HUMAN	zp98c09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562 G806562 NEBULIN. ;
7203	17080	27266	1.36	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
7203	17080	27267	1.36	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5681	15590	25692	4.29	9.0E-99	AW968635.1	EST_HUMAN	EST380711 MAGE resequences, MAGJ Homo sapiens cDNA
8465	18338	28602	2.6	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
8465	18338	28603	2.6	9.0E-99	AI479829.1	EST_HUMAN	tm69h07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BID_HUMAN P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
8716	18533	28817	1.84	9.0E-99	AA134604.1	EST_HUMAN	zn90d02.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G662994 G662994 GPI-ANCHORED PROTEIN P137. ;
7065	16942	27134	1.19	8.0E-99	9635487	NT	Human endogenous retrovirus, complete genome
5561	15477	25550	9.2	7.0E-99	AF035808.1	NT	Homo sapiens oscillin (hLn) gene, exon 5
8884	18695	28988	2.31	7.0E-99	AF001886.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
2080	11970	21863	0.93	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
2080	11970	21864	0.93	6.0E-99	11430555	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
3814	13726	23517	1.87	6.0E-99	AW976364.1	EST_HUMAN	EST388473 MAGE resequences, MAGN Homo sapiens cDNA
4642	14530	24318	1.16	6.0E-99	4502660	NT	Homo sapiens CD34 antigen (CD34) mRNA
6013	15917	26047	2.36	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6013	15917	26048	2.36	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6718	16598	26787	1.21	6.0E-99	X99101.1	NT	H.sapiens mRNA for estrogen receptor
7089	16966	27160	2.18	6.0E-99	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
7143	17020	27213	3.57	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
7143	17020	27214	3.57	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
8102	17992	28241	3.72	6.0E-99	11526299	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
902	10827	20671	0.86	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
902	10827	20672	0.86	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
1922	11817	21696	2.36	5.0E-99	Y11365.1	NT	H.sapiens IMPA gene, exon 8
4463	14357	24148	1.35	5.0E-99	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
5066	14936	24709	2.46	5.0E-99	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
9360	19032		2.1	5.0E-99	BE890177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6844	16723		5.37	3.0E-99	M95586.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1219	11128		3.46	2.0E-99	AW274792.1	EST_HUMAN	xp09e06.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3220	13144	22947	1.08	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4443	14337	24127	3.15	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7053	16930	27121	9.75	2.0E-99	W23507.1	EST_HUMAN	zb46d06.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
8451	18324	28583	3.83	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
312	10274	20093	1.53	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
375	10329	20152	1.04	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1401	11306	21166	2.11	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1537	11441	21298	1.47	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1537	11441	21299	1.47	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1885	11781	21656	1.1	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1885	11781	21657	1.1	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3046	12973	22766	0.89	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4283	14182	23960	2.74	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4283	14182	23961	2.74	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
5200	15063		1.18	1.0E-99	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
7305	17181		1.15	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
7483	17353	27557	1.68	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711 O02711 PRO-POL-DUTPASE POLYPROTEIN ;
8683	18571	28854	2.4	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
9125	18884		3.76	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	9989	19780	1.13	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	9989	19780	1.93	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
62	10048	19859	1.48	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
62	10048	19860	1.48	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
81	10065	19883	1.52	1.0E-100	AW275237.1	EST_HUMAN	xv78b11.x1 NCI_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2824605 3'
162	10135	19950	1.16	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
314	10276	20095	1.01	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
340	10299	20114	2.43	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
430	10375		1.53	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
481	10425		7.04	1.0E-100	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
500	10442	20255	4.17	1.0E-100	BE180609.1	EST_HUMAN	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
1002	10920	20763	2.43	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1002	10920	20764	2.43	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1528	11433		1.33	1.0E-100	AW207555.1	EST_HUMAN	UI-H-BI1-afk-c-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1533	11437	21294	1.46	1.0E-100	AI200857.1	EST_HUMAN	qf62f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA P81061 CYSTATIN ;
2195	12082		1.45	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2388	12267	22160	1.08	1.0E-100	X62468.1	NT	H.sapiens mRNA for IFN-gamma (pKC-0)
2674	12539	22429	1.87	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2985	12913		2.45	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4116	14016	23796	1.49	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4143	14043	23816	1.87	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5024	14897	24665	3.07	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5024	14897	24666	3.07	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5232	15156	24924	1.8	1.0E-100	BF244218.1	EST_HUMAN	601863164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5496	15415	25478	1.4	1.0E-100	AU118182.1	EST_HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5514	15432	25496	1.55	1.0E-100	AF135116.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
5915	15821	25946	5.1	1.0E-100	AU140214.1	EST_HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6015	15919	26049	1.41	1.0E-100	R10887.1	EST_HUMAN	yf38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6116	16010	26146	1.4	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6116	16010	26147	1.4	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
6119	16013	26151	6.99	1.0E-100	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
6963	16841	27033	6.19	1.0E-100	BF103853.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3931310 5'
6983	16860		5.44	1.0E-100	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7322	17198	27398	3.2	1.0E-100	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7369	17347		1.53	1.0E-100	AI972388.1	EST_HUMAN	wr37g09.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element MER22 repetitive element ;
7426	16439	26625	1.67	1.0E-100	AW998611.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
7527	17378	27587	1.73	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7527	17378	27588	1.73	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7664	17514	27740	1.69	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7664	17614	27741	1.69	1.0E-100	AW630487.1	EST_HUMAN	hh83c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
8016	17866		1.29	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
8141	18029	28275	5.23	1.0E-100	BF327292.1	EST_HUMAN	MR0-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
8606	18473	28745	2.14	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
8606	18473	28746	2.14	1.0E-100	X94633.1	NT	H.sapiens CD97 gene exon 4
8660	18549	28831	4.56	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8660	18549	28832	4.56	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
8688	9989	19780	1.96	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8930	18738		1.86	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
9048	18832	29114	5.59	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9351	19027	25302	2.21	1.0E-100	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9940	19409	25181	3.38	1.0E-100	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
70	10055	19871	1.22	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
70	10055	19872	1.22	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
671	10605	20422	1.16	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
688	10621	20447	4.45	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
688	10621	20448	4.45	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
754	10684	20521	1.32	1.0E-101	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
835	10762	20612	1.28	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
908	10832	20679	3.44	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
969	10892	20741	12.74	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297291 5'
1036	10954	20796	1.63	1.0E-101	AI221878.1	EST_HUMAN	qg99e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1712	11613	21483	0.87	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1712	11613	21484	0.87	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1901	11797	21677	1.62	1.0E-101	4502996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2010	11902	21792	1.6	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160600-016-h09 ST0281 Homo sapiens cDNA
2301	12718	22080	1.66	1.0E-101	5729892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2572	12443	22335	4.4	1.0E-101	X72993.1	NT	H.sapiens EWS gene, exon 5
2714	12576	22468	2.56	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2714	12576	22469	2.56	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2925	12852		12.14	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3167	13092	22897	2.51	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3203	13127		2.16	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3334	13254	23059	1.67	1.0E-101	AW965556.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
3354	12576	22468	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3354	12576	22469	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3800	13712	23499	4.83	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4965	14840	24609	1.67	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
4965	14840	24610	1.67	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5257	15179	24954	1.4	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGE resequences, MAGI Homo sapiens cDNA
5651	15563	25658	3.73	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5651	15563	25659	3.73	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6333	16196	26356	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6333	16196	26357	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6416	16278	26441	5.63	1.0E-101	AW008475.1	EST_HUMAN	wv55f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
6471	16330		1.56	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349901 5'
6544	16402	26581	5.3	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-f12 BT0313 Homo sapiens cDNA
6693	16573	26764	2.65	1.0E-101	BF029174.1	EST_HUMAN	601764686F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'
7208	17085	27274	1.15	1.0E-101	AA036800.1	EST_HUMAN	zk29g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast ;
7446	16458	26650	16.52	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
7446	16458	26651	16.52	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
7454	17263	27468	18.4	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7623	17474	27694	5.64	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7623	17474	27695	5.64	1.0E-101	BE619667.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
7950	17800	28040	1.76	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
8252	18132	28381	2.88	1.0E-101	S38327.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
8454	18327	28586	1.78	1.0E-101	AB020626.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
9610	19189		11.62	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
338	10297	20111	3.24	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
604	10540	20350	0.89	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
758	10688	20526	1.46	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1101	11017	20859	1.95	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1247	11154	21002	1.39	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1247	11154	21003	1.39	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1398	11303	21162	90.24	1.0E-102	BE408447.1	EST_HUMAN	601299982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'
2261	12145	22044	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
2261	12145	22045	1.34	1.0E-102	AI124669.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
3026	12954	22747	1.51	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3094	13021	22815	5.61	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3094	13021	22816	5.61	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4139	14039	23814	1.46	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4314	14211	23994	2.11	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5063	14933	24705	1.09	1.0E-102	R66488.1	EST_HUMAN	yi32c04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5300	15221	25025	1.88	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5515	15433		7.27	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5536	15453	25522	3.46	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5536	15453	25523	3.46	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5800	15706	25818	2.54	1.0E-102	AI459825.1	EST_HUMAN	ar82f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52. ;
6351	16214	26376	6.56	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
6495	16354	26524	2.53	1.0E-102	AV710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuAAKD03 5'
6787	16666	26867	4.2	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-h08 NT0025 Homo sapiens cDNA
6832	16711	26904	2.53	1.0E-102	BE910555.1	EST_HUMAN	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'
6945	16823	27014	1.36	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
6945	16823	27015	1.36	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEEE11 5'
7001	16878	27069	4.06	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7374	17243	27448	1.52	1.0E-102	T70393.1	EST_HUMAN	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
7374	17243	27449	1.52	1.0E-102	T70393.1	EST_HUMAN	yd13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
7415	17282	27490	3.58	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
7961	17811	28052	2.03	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
7961	17811	28053	2.03	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
7981	17831	28070	2.9	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
7981	17831	28071	2.9	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
8005	17855	28096	2.3	1.0E-102	AA970786.1	EST_HUMAN	cn57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2. [1] ;
8421	18295	28549	2.38	1.0E-102	BE897468.1	EST_HUMAN	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8424	18298	28553	1.99	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8424	18298	28554	1.99	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8708	18525	28807	2.78	1.0E-102	BF359243.1	EST_HUMAN	RC6-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
8947	18755	29051	4.04	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
9054	18837		2.82	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9601	19183	25247	4.77	1.0E-102	AW300862.1	EST_HUMAN	xk07c12.x1 NCI_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2666038 3'
63	10049	19861	0.82	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
63	10049	19862	0.82	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
93	10078	19894	8.1	1.0E-103	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
201	10173	19989	0.83	1.0E-103	5453793	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
965	10888	20734	1.01	1.0E-103	AJ278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1223	11131	20985	7.29	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1578	11482	21342	2.32	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
1872	11768	21643	1.04	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
1932	11827	21708	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1932	11827	21709	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2257	12141	22040	1.57	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'
2401	12278	22175	2.22	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2578	12449	22340	0.86	1.0E-103	N32770.1	EST_HUMAN	yw91d08.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259599 3'
3030	12958		2.43	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3333	13253	23058	3.44	1.0E-103	AW298245.1	EST_HUMAN	UI-H-BW0-ajt-h-11-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3393	13310	23108	1.06	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3695	13609		2.41	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3725	13637	23423	1.16	1.0E-103	AA485663.1	EST_HUMAN	ab10d12.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
3757	13670	23454	1.39	1.0E-103	11430876	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
3922	13831	23611	3.02	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
5619	15534	25619	1.72	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
5998	15903	26027	5.37	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6033	15936	26069	1.68	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6033	15936	26070	1.68	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
6092	15102	24878	1.68	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6092	15102	24879	1.68	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6289	16153	26310	1.64	1.0E-103	AW965776.1	EST_HUMAN	EST377849 MAGE resequences, MAGI Homo sapiens cDNA
6338	16201	26361	3.21	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
6568	16426	26607	3.28	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
6568	16426	26608	3.28	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS. ;
6823	16702	26896	2.95	1.0E-103	T31080.1	EST_HUMAN	EST27193 Human Brain Homo sapiens cDNA 5' end similar to None
7010	16887	27079	1.17	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7010	16887	27080	1.17	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
7050	16927	27118	1.43	1.0E-103	BF109244.1	EST_HUMAN	7l60e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
7267	17144	27337	3.08	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7267	17144	27338	3.08	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7787	17637	27870	2.02	1.0E-103	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7815	17665	27905	2.09	1.0E-103	AW963676.1	EST_HUMAN	EST375749 MAGE resequences, MAGH Homo sapiens cDNA
7878	17728	27972	9.93	1.0E-103	AI878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O15046 KIAA0338 ;
8115	18004	28260	3.08	1.0E-103	AI792759.1	EST_HUMAN	ol02d06.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
8218	18101	28353	2.74	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8218	18101	28354	2.74	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8681	18569	28852	2.56	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
8743	17892	28136	6.49	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8973	18778	29070	3.42	1.0E-103	BE644611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.t3 MER29 repetitive element ;

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9049	18833		1.72	1.0E-103	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9079	18855		2.65	1.0E-103	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9275	18979	25323	2.21	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
233	10202	20016	2.6	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
233	10202	20017	2.6	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1845	11741	21617	1.81	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2147	12035	21932	7.16	1.0E-104	AA132975.1	EST_HUMAN	zo22c06.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116_rna1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2157	12044	21944	1.91	1.0E-104	BE744628.1	EST_HUMAN	601577460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2318	12199	22097	1.15	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2318	12199	22098	1.16	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2387	12266	22159	1.55	1.0E-104	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2842	12770	22559	7.64	1.0E-104	M34671.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2886	12813		2.82	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II
3345	13265		1.54	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3550	13465	23260	0.99	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3550	13465	23261	0.99	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3861	13772	23564	0.91	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4280	14179	23957	4.28	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4504	14397	24182	0.9	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4504	14397	24183	0.9	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5617	15532	25615	1.33	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5617	15532	25616	1.33	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
5891	15797	25919	8.46	1.0E-104	AI768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN. ;contains element LTR7 repetitive element ;
5891	15797	25920	8.46	1.0E-104	AI768797.1	EST_HUMAN	wj03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN. ;contains element LTR7 repetitive element ;
6073	16056	26204	1.52	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6073	16056	26205	1.52	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6288	16152	26309	2.38	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7288	17164	27363	2.24	1.0E-104	BF448230.1	EST_HUMAN	nad16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
7370	17239	27442	4.66	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
7370	17239	27443	4.66	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7430	16443	26630	3.84	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
7430	16443	26631	3.84	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
7809	17659	27898	3.14	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7809	17659	27899	3.14	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7947	17797	28037	1.42	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
7966	17816	28057	4.51	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
8014	17864	28110	4.24	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
8617	18484	28755	1.84	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
8617	18484	28756	1.84	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
8641	18505	28783	4.49	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
9842	19340		1.37	1.0E-104	BE393692.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658676 5'
277	12637	20062	2.86	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
419	9986	19777	16.85	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
579	10517	20323	3.22	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
579	10517	20324	3.22	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1777	11676	21553	1.16	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1884	11780	21655	1.75	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2142	12030	21928	1.64	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2689	12554		0.87	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
2975	12902		2.57	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3307	13228	23032	0.93	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3307	13228	23033	0.93	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3592	13506		1.26	1.0E-105	11425532	NT	Homo sapiens dermatopontin (DPT), mRNA
4008	13914	23689	2.15	1.0E-105	AW961688.1	EST_HUMAN	EST373761 MAGE resequences, MAGG Homo sapiens cDNA
4638	14526	24313	0.84	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4638	14526	24314	0.84	1.0E-105	BE868881.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4855	14735		3.74	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5044	14916	24690	0.95	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
5095	14965	24740	2.23	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5161	14916	24690	1.3	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
6167	15124	24840	3.06	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6167	15124	24841	3.06	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6679	16559	26754	6.43	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCR32

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6894	16773	26967	1.8	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2500626 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
7234	17111	27304	2.99	1.0E-105	AW016879.1	EST_HUMAN	UI-H-BI0p-abl-b-12-0-UI.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
8303	18181	28428	5.44	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
8560	18430	28699	1.8	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 31
8602	18469	28740	2.06	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
8867	18679	28968	2.01	1.0E-105	AW027554.1	EST_HUMAN	wv74f07.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892 P87892 PROTEASE ;
145	10119		0.96	1.0E-106	AW503208.1	EST_HUMAN	UI-HF-BN0-akt-g-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
198	10170	19987	1.54	1.0E-106	AI565065.1	EST_HUMAN	tq79c01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2215008 3'
531	10473	20286	1.77	1.0E-106	AW965556.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
589	10527	20334	0.79	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
590	10527	20334	1.21	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1508	11413	21272	2.66	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1674	11576	21444	4.51	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1762	11661	21533	5.12	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
1762	11661	21534	5.12	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element ;
2075	11965	21858	1.08	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2269	12153	22052	8.39	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2456	12333	22229	1.63	1.0E-106	AF003528.1	NT	Homo sapiens X-linked anhidroltic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2557	12429	22322	1.25	1.0E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2559	12431	22324	1.94	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2729	12591	22487	4.23	1.0E-106	AI276526.1	EST_HUMAN	ql76h10.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2795	11319	21183	2.97	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2795	11319	21184	2.97	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2911	12837	22635	5.01	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2911	12837	22636	5.01	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3143	13068	22867	2.36	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3143	13068	22868	2.36	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3328	13248	23053	0.8	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3394	13311	23109	0.98	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3394	13311	23110	0.98	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3952	13860	23634	7.22	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
3952	13860	23635	7.22	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
4497	14391	24176	1.21	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5183	15047		1.21	1.0E-106	L41644.1	NT	Homo sapiens dystrophin gene, exon 41
5298	15219	25022	2.98	1.0E-106	AA781155.1	EST_HUMAN	aj24b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5711	15619	25722	6.78	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295067 5'
5866	15772	25891	16.4	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5866	15772	25892	16.4	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6361	16224	26385	5.59	1.0E-106	AA663779.1	EST_HUMAN	ae72e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
6390	16252	26412	4.83	1.0E-106	11429617	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
6431	16292	26453	1.35	1.0E-106	BE292722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
6490	16348	26517	7.6	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
6490	16348	26518	7.6	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
6657	16537	26733	5.33	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
6657	16537	26734	5.33	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
6754	16633	26821	1.48	1.0E-106	AI523066.1	EST_HUMAN	ar68a07.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);
7052	16929	27120	3.16	1.0E-106	AI654123.1	EST_HUMAN	ty62a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICA6_HUMAN Q05084 69 KD ISLET CELL AUTOANTIGEN ;
7281	17158	27353	1.86	1.0E-106	AA825307.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7281	17158	27354	1.86	1.0E-106	AA825307.1	EST_HUMAN	oc67e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7351	17219	27419	2.79	1.0E-106	AI750447.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03a04 random
7424	17291	27501	1.86	1.0E-106	AI479569.1	EST_HUMAN	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element ;
7424	17291	27502	1.86	1.0E-106	AI479569.1	EST_HUMAN	tm41f02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.t3 TAR1 PTR5 repetitive element ;
7803	17653	27890	1.32	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
7803	17653	27891	1.32	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
7880	17730	27975	5.83	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
7880	17730	27976	5.83	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7901	17751	27990	1.86	1.0E-106	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
8019	17869	28113	3.66	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8269	18149	28389	5.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
8269	18149	28390	5.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
8415	18289	28544	2.28	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
8415	18289	28545	2.28	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
9122	19540		2.87	1.0E-106	AW410405.1	EST_HUMAN	fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961644 5'
9342	19022	25298	2.31	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9342	19022	25299	2.31	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9554	19152		5.35	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
234	10203		3.48	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
264	10229		1.05	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
606	10542		1.07	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
614	10550	20361	1.7	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
796	10725	20565	0.86	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
868	10794	20644	1.16	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
953	10877	20724	10.67	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1267	11164	21016	0.78	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1551	11456	21314	2.13	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1718	11619	21488	1.47	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1797	11695	21571	0.95	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1797	11695	21572	0.95	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2161	12048	21949	1.26	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2487	12362	22257	0.86	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2487	12362	22258	0.86	1.0E-107	BE732460.1	EST_HUMAN	601567619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2976	12903	22701	1.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2976	12903	22702	1.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3061	12988	22779	2.62	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
3754	13667	23450	3.92	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5575	15490	25567	3.26	1.0E-107	BE867469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846494 5'
6356	16219	26380	1.52	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
6356	16219	26381	1.52	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-alf-c-08-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
6445	16306	26471	1.63	1.0E-107	AI765078.1	EST_HUMAN	wh56h04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8087	17978	28228	2.73	1.0E-107	AI392850.1	EST_HUMAN	tg10d06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI P05095 ALPHA-ACTININ 3, NON MUSCULAR ;
8316	18193	28443	1.82	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
8327	18204	28453	1.98	1.0E-107	BF666511.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
8638	18503	28779	9.12	1.0E-107	BE540550.1	EST_HUMAN	601066681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
8697	17881	28122	4.21	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
8697	17881	28123	4.21	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
9187	19673		3.94	1.0E-107	AA001415.1	EST_HUMAN	ze45e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1 THR repetitive element ;
939	10864	20711	1.46	1.0E-108	BE296042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1244	11151	20999	1.55	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2282	12166	22063	7.41	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2282	12166	22064	7.41	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2378	12258	22160	7.2	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3305	13226	23028	0.94	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3305	13226	23029	0.94	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3742	13654	23437	0.92	1.0E-108	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4065	13967	23744	1.33	1.0E-108	AW664438.1	EST_HUMAN	hi12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1. ;
4425	14320	24106	1.99	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4425	14320	24107	1.99	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4699	14585	24376	2.85	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4868	14748	24528	2.19	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5366	15286	25120	1.53	1.0E-108	AW384094.1	EST_HUMAN	RC0-HT0372-241199-031-d03 HT0372 Homo sapiens cDNA
5393	15312	25166	2.77	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5393	15312	25167	2.77	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5732	15640	25745	5.06	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
5732	15640	25746	5.06	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5789	15695	25804	1.37	1.0E-108	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6247	16113	26265	5.35	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA
6399	16260	26421	3.34	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADSD6) mRNA
6698	16578		1.93	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8202	15099	24891	2.77	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
8593	18461	28731	4.26	1.0E-108	AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
8677	18565		2.03	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
8706	12166	22063	4.14	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8706	12166	22064	4.14	1.0E-108	AI686040.1	EST_HUMAN	tt91e10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
9357	19030	25303	2.79	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
9736	19270		5.59	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154297 5'
58	10044	19856	0.9	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
212	10183	19997	0.92	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
222	10192	20003	1.51	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
459	10403	20219	3.64	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2) mRNA
583	10521	20328	14.64	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
583	10521	20329	14.64	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1184	11095	20941	9.63	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1185	11095	20941	4.89	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1831	11728	21602	1.48	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2194	12081	21985	2.03	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2204	12091	21993	1.97	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2581	12452	22344	3.88	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;
2581	12452	22345	3.88	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:O02197 O02197 CIRCULATING CATHODIC ANTIGEN. ;
2682	12463	22346	2.75	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3020	12948	22740	1.88	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3342	13262	23068	1.45	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3342	13262	23069	1.45	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3474	13390	23195	1.2	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3767	13680		1.53	1.0E-109	BE146144.1	EST_HUMAN	MR0-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
3911	13821	23601	1.54	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3911	13821	23602	1.54	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4054	13956	23732	3.67	1.0E-109	AI655417.1	EST_HUMAN	ts98e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE16100 ;
4070	13972	23749	1.02	1.0E-109	AA662274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2 ;
4070	13972	23750	1.02	1.0E-109	AA662274.1	EST_HUMAN	nu93c12.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW:GTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2 ;
4304	14202	23986	2.25	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4496	14390	24175	1.19	1.0E-109	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4839	14720	24503	1.04	1.0E-109	R15400.1	EST_HUMAN	ya48e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
4984	14859	24626	0.86	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
4984	14859	24627	0.86	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
5254	15176	24950	2.31	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
5648	15364		1.48	1.0E-109	BE179356.1	EST_HUMAN	RC1-HT0615-200400-022-d04 HT0615 Homo sapiens cDNA
6465	16325	26491	3.66	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6466	16326	26492	5.01	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6466	16326	26493	5.01	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6753	16632	26820	1.36	1.0E-109	AL049784.1	NT	Novel human gene mapping to chomosome 13
6820	16699	26892	1.23	1.0E-109	AW749130.1	EST_HUMAN	PM0-BT0340-091299-002-e05 BT0340 Homo sapiens cDNA
7030	16907		1.72	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7071	16948	27139	5.71	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
7071	16948	27140	5.71	1.0E-109	BE787540.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
7326	17202	27402	2	1.0E-109	H84860.1	EST_HUMAN	ys90g08.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP:A53491 A53491 BUMETANIDE-SENSITIVE NA-K-C1 COTRANSPORTER - SPINY ;
7462	17322	27528	1.41	1.0E-109	F06604.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-1ec12
8155	18043	28294	2.93	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
8155	18043	28295	2.93	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
8183	18069	28318	14.2	1.0E-109	BF694831.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
8335	18212	28464	2.12	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
8335	18212	28465	2.12	1.0E-109	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
8468	18341	28606	1.88	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8676	18564	28848	2.19	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
8710	18527	28810	4.83	1.0E-109	W16510.1	EST_HUMAN	zb08b12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat ;
9259	12091	21993	1.65	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
9594	19176	25275	2.8	1.0E-109	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3	9990	19781	1.48	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
34	10021	19817	3.88	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
34	10021	19818	3.88	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
75	10059	19876	30.63	1.0E-110	C04498.1	EST_HUMAN	C04498 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC3467
104	9990	19781	1.67	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
291	10255	20076	0.91	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
516	10458	20269	1.16	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1163	11076	20921	1.09	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1258	11165	21016	1.01	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1879	11775	21650	1.5	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2012	11904		1.86	1.0E-110	BF508896.1	EST_HUMAN	UI-H-BI4-aos-b-05-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2810	12739		1.02	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3048	12975		1.07	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3158	13083	22885	1.87	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3158	13083	22886	1.87	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3966	13873	23650	0.92	1.0E-110	BE018556.1	EST_HUMAN	bb82a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312 KIAA0566 PROTEIN ;
4533	14426	24207	2.06	1.0E-110	AI017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to SW:N121_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4555	14447	24232	2.08	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
4898	14778		2.34	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5237	15161	24929	1.9	1.0E-110	BE299406.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5511	15429	25492	7.34	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5511	15429	25493	7.34	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6032	19458	26068	4.36	1.0E-110	M55112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
6391	16253	26413	10.04	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
6391	16253	26414	10.04	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCGE01 5'
6409	16270	26432	2.7	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7523	17374	27583	2.91	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
7915	17765	28004	4.27	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
8130	18018	28266	3.7	1.0E-110	Y12337.1	NT	H.sapiens mRNA for myotonic dystrophy protein kinase like protein
8334	18211	28462	3.49	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
8334	18211	28463	3.49	1.0E-110	BE734357.1	EST_HUMAN	601565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
8740	17889	28133	2.43	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 G1145816 FKBP54 ;
9081	18857		4.15	1.0E-110	BE897218.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
9204	18935		5.78	1.0E-110	AW062258.1	EST_HUMAN	IL0-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
9444	19080		1.63	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9578	19684		5.07	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
168	10140		16.85	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
189	10161	19978	1.02	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
718	10650		1.87	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
726	10658	20489	3.58	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
911	10835	20684	73.62	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3642	13556	23342	1.17	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3642	13556	23343	1.17	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4080	13982	23760	1.08	1.0E-111	7661569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4235	14133	23909	4.45	1.0E-111	K02268.1	NT	Human enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds
5364	15284	25117	2.82	1.0E-111	AA151017.1	EST_HUMAN	zl47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5364	15284	25118	2.82	1.0E-111	AA151017.1	EST_HUMAN	zl47b07.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5675	15584	25685	1.71	1.0E-111	AI344679.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6402	16263	26423	3.03	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
6579	16437	26622	2.29	1.0E-111	AA133914.1	EST_HUMAN	zn62c12.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562774 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
6795	16674	26866	3.13	1.0E-111	U66533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
7113	16990		10.8	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
7149	17026	27221	13.75	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
7149	17026	27222	13.75	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
7251	17128	27321	3.26	1.0E-111	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7840	17690	27935	1.51	1.0E-111	AA504160.1	EST_HUMAN	aa58g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
7893	17743	27986	6.35	1.0E-111	AA131248.1	EST_HUMAN	zl31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
8401	18277	28529	4.52	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
9038	18825	29110	3.04	1.0E-111	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9686	19489	25130	1.69	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
9959	19422	25171	1.39	1.0E-111	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9959	19422	25172	1.39	1.0E-111	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
592	10528	20335	2.66	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
594	10530	20337	4.49	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
594	10530	20338	4.49	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
616	10552	20363	1.48	1.0E-112	BF509039.1	EST_HUMAN	UI-H-BI4-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
616	10552	20364	1.48	1.0E-112	BF509039.1	EST_HUMAN	UI-H-BI4-aot-g-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
985	10908	20753	2.78	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1046	10964	20805	1.72	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1658	11560	21424	5.88	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1658	11560	21425	5.88	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2460	12337	22231	2.45	1.0E-112	BE866859.1	EST_HUMAN	601442674F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3809	13721	23510	0.83	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-f09 BT0590 Homo sapiens cDNA
4646	14533	24321	5.12	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4646	14533	24322	5.12	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5170	15036	24804	0.94	1.0E-112	9055269	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDIT), mRNA
5477	15397	25463	33.34	1.0E-112	N46046.1	EST_HUMAN	yy35d07.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6340	16203	26364	1.81	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
6340	16203	26365	1.81	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
6766	16646	26834	1.65	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
7181	17058	27247	2.25	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7181	17058	27248	2.25	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
7693	17543	27767	2.09	1.0E-112	BF111413.1	EST_HUMAN	7l30g07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN. ;
8159	18047	28299	4.25	1.0E-112	AW863327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
8318	18195	28445	2.86	1.0E-112	AJ249900.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8445	18319	28578	1.72	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
8500	18373	28637	1.75	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
8500	18373	28638	1.75	1.0E-112	AI792603.1	EST_HUMAN	qk24c08.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
8521	18393	28657	5	1.0E-112	AW377670.1	EST_HUMAN	PM0-CT0237-141099-001-h02 CT0237 Homo sapiens cDNA
725	10657	20487	3.71	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
725	10657	20488	3.71	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
927	10852	20700	6.32	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1523	11428	21286	2.94	1.0E-113	AI365586.1	EST_HUMAN	ao95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
2048	11939	21833	1.18	1.0E-113	BF515218.1	EST_HUMAN	UI-H-BW1-anl-f-03-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
2405	12282	22179	0.96	1.0E-113	AJ006976.1	NT	Homo sapiens PLP gene
3091	13018	22813	2.34	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5035	14907	24677	0.95	1.0E-113	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5035	14907	24678	0.95	1.0E-113	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5211	19524		16.27	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5377	15297	25144	6.33	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
5608	15523	25605	3.92	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
5699	15608	25710	2.05	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7257	17134	27326	2.95	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7257	17134	27327	2.95	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7656	17506	27731	1.29	1.0E-113	11429367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
8466	18339	28604	1.73	1.0E-113	AW500519.1	EST_HUMAN	UI-HF-BN0-akj-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
8550	15719	25832	2.07	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8550	15719	25833	2.07	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8584	18452	28721	3.44	1.0E-113	BE292968.1	EST_HUMAN	601105529F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2988366 5'
629	10566	20379	7.66	1.0E-114	T70551.1	EST_HUMAN	yd15c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);contains Alu repetitive element;
1055	10972	20815	1.31	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1291	11198	21053	3.47	1.0E-114	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1648	11652	21413	5.63	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2773	10025	19823	0.82	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2773	10025	19824	0.82	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3092	13019	22814	2.29	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3135	13060	22859	1.2	1.0E-114	BF206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3934	13843	23621	1.95	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5120	14988	24762	1.2	1.0E-114	AA194468.1	EST_HUMAN	zq05e05.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628832 5' similar to contains MER22.t3 MER22 repetitive element ;
5121	14989	24763	2.31	1.0E-114	AF004849.1	NT	Homo sapiens PKY protein kinase mRNA, complete cds
5316	15237	25040	1.37	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5316	15237	25041	1.37	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
6316	16179	26338	7.08	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6316	16179	26339	7.08	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6606	16486	26673	1.86	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
6748	16627	26814	1.73	1.0E-114	AI363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
6748	16627	26815	1.73	1.0E-114	AI363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'
7048	16925	27116	3.39	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
7090	16967	27161	6.35	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
7090	16967	27162	6.35	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
7418	17285		3.79	1.0E-114	AW327455.1	EST_HUMAN	dq03f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
7447	16459	26652	3.13	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
7844	17694	27940	1.31	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8167	18055		7.14	1.0E-114	BE302666.1	EST_HUMAN	ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
8527	18399	28666	4.58	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
8527	18399	28667	4.58	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
8834	18647	28932	2.86	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
8834	18647	28933	2.86	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cdA Homo sapiens cDNA clone cdABA08 5'
9479	19748		3.21	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
9729	19266	25222	3.06	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
9729	19266	25223	3.06	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
21	10008	19801	3.36	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
125	10099	19920	0.95	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
129	10103		1.99	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
289	10253	20073	2.17	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
525	10467	20278	1.08	1.0E-115	AI339206.1	EST_HUMAN	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
525	10467	20279	1.08	1.0E-115	AI339206.1	EST_HUMAN	qt06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
769	10699	20537	1.83	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
769	10699	20538	1.83	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
771	10701	20540	49.82	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1539	11443	21301	0.92	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1539	11443	21302	0.92	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1785	11683	21561	3.14	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1798	11696	21573	1.42	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2034	11925	21817	0.87	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2034	11925	21818	0.87	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2820	12749		1.76	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
3077	13004	22795	2.1	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3077	13004	22796	2.1	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3427	13344	23149	4.03	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
3956	13864	23640	4.04	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4169	14069	23844	1.09	1.0E-115	AL137163.1	NT	Novel human gene mapping to chomosome X
4301	14199	23983	3.41	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4335	14232	24014	3.83	1.0E-115	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4578	14468	24254	2.58	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4578	14468	24255	2.58	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4813	14696	24482	2.96	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4813	14696	24483	2.96	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5279	15201	24977	1.75	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE resequences, MAGK Homo sapiens cDNA
5330	15250	25055	7.22	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5402	15321	25369	2.05	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5402	15321	25370	2.05	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5852	15758	25876	12.92	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
5933	15838	25960	1.93	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5933	15838	25961	1.93	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6313	16176	26333	1.55	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
6313	16176	26334	1.55	1.0E-115	AI076598.1	EST_HUMAN	oz31a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
6379	16241	26401	7.41	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
6744	16623	26811	12.78	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6744	16623	26812	12.78	1.0E-115	BE830187.1	EST_HUMAN	RC6-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
7116	16993	27184	2.2	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
7745	17595	27816	1.92	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
7745	17595	27817	1.92	1.0E-116	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
8100	17990	28239	3.5	1.0E-115	AW571544.1	EST_HUMAN	xx32f08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAYP_CANFA P10463 CALCYPHOSINE ;
8701	18519	28801	2.26	1.0E-115	4502528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
560	10500	20306	1.42	1.0E-116	BE275502.1	EST_HUMAN	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988876 5'
783	10713	20552	1.25	1.0E-116	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
841	10768		6.89	1.0E-116	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
1952	11847	21733	2.38	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1952	11847	21734	2.38	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1980	11873	21765	1.21	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2050	12711	21834	1.01	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2050	12711	21835	1.01	1.0E-116	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2259	12143	22042	1.88	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2293	12175		1.49	1.0E-116	U78308.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2407	12284	22181	4.48	1.0E-116	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2704	12656	22458	2.19	1.0E-116	BE889256.1	EST_HUMAN	601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3137	13062	22860	4.73	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3137	13062	22861	4.73	1.0E-116	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4281	14180	23958	2.01	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4747	14632	24418	2.17	1.0E-116	AI907096.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5122	14990	24764	1.2	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5637	15550	25641	5.88	1.0E-116	W42822.1	EST_HUMAN	zc24d07.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
5768	15675	25781	1.65	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds

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5768	15675	25782	1.65	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
5853	15759	25877	72.79	1.0E-116	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
5924	15829		1.8	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0379-210200-102-b04 HT0379 Homo sapiens cDNA
6145	16018	26156	3.59	1.0E-116	C02944.1	EST_HUMAN	C02944 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC0567
6275	16139	26295	7.97	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCBBCG06 5'
6874	16753	26949	1.99	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
6874	16753	26950	1.99	1.0E-116	AA354256.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
7173	17050	27239	1.43	1.0E-116	BE565507.1	EST_HUMAN	601338268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680680 5'
7260	17137	27330	1.98	1.0E-116	AI216352.1	EST_HUMAN	qh09c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X53741_rna1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7577	17428	27642	1.77	1.0E-116	11418646	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
8074	17965	28216	3.68	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-e06 CT0482 Homo sapiens cDNA
8477	18350	28615	3.23	1.0E-116	AI367140.1	EST_HUMAN	qq41e04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7 CE01765 ;
9591	19741		2.08	1.0E-116	BE258569.1	EST_HUMAN	601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344580 5'
9776	19614		2.68	1.0E-116	AL134889.1	EST_HUMAN	DKFZp762L1110_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762L1110 5'
546	10487	20296	1.18	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1061	12684	20821	1.59	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1719	11620	21489	6.25	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1790	11688	21564	2.3	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2164	12051	21952	2.99	1.0E-117	AW957699.1	EST_HUMAN	EST369769 MAGE resequences, MAGE Homo sapiens cDNA
3230	13154	22953	1.75	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
3908	13818	23599	3.62	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4247	14146	23920	1.86	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4475	14369	24158	1.88	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4622	14510	24299	1.36	1.0E-117	X89670.1	NT	H.sapiens mRNA for TPCR16 protein
4622	14510	24300	1.35	1.0E-117	X89670.1	NT	H.sapiens mRNA for TPCR16 protein
4705	14591	24382	9.22	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4705	14591	24383	9.22	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4856	14736	24516	3.36	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5280	15202	24978	2.5	1.0E-117	BE730508.1	EST_HUMAN	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6404	16265	26426	4.99	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
6404	16265	26427	4.99	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds

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6455	16316	26482	3.77	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6455	16316	26483	3.77	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6651	16531	26725	5.93	1.0E-117	AI950145.1	EST_HUMAN	wp86b07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065 O75065 KIAA0477 PROTEIN. ;
6837	16716	26908	1.7	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
6837	16716	26909	1.7	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
7361	17228	27428	2.28	1.0E-117	D16524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
7635	17486	27706	1.51	1.0E-117	BE733922.1	EST_HUMAN	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
8385	18262	28512	10.31	1.0E-117	W80605.1	EST_HUMAN	zd83b11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:347229 5' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8595	18462	28732	3.96	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
8595	18462	28733	3.96	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
8698	18516		15.63	1.0E-117	BE269856.1	EST_HUMAN	601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544296 5'
8872	18684	28974	2.22	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8872	18684	28975	2.22	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
64	10050	19863	9.54	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
90	10074	19890	2.59	1.0E-118	AL045854.1	EST_HUMAN	DKFZp434I056_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I056 5'
506	10448	20261	5.09	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
896	12680	20667	0.98	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2186	12073	21975	2.39	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2186	12073	21976	2.39	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2186	12073	21977	2.39	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2281	12165		3.77	1.0E-118	AW951729.1	EST_HUMAN	EST363799 MAGE resequences, MAGB Homo sapiens cDNA
2711	12574	22465	2.38	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2711	12574	22466	2.38	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3066	12993		3.73	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3159	13084	22887	4.51	1.0E-118	AI347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3159	13084	22888	4.51	1.0E-118	AI347694.1	EST_HUMAN	qp01f05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3998	13904	23679	7.67	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
5329	15249	25053	2.02	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5329	15249	25054	2.02	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5620	15535	25620	1.88	1.0E-118	11420764	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6020	15924	26054	1.87	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6020	15924	26055	1.87	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6482	16341	26509	4.13	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
6648	16528	26722	2.23	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
6884	16763	26960	7.81	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6884	16763	26961	7.81	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
6888	16767	26963	1.34	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
6888	16767	26964	1.34	1.0E-118	AA443024.1	EST_HUMAN	zx98d07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
7035	16912	27100	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
7035	16912	27101	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
7062	16939	27129	1.28	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7062	16939	27130	1.28	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7223	17100	27288	5.71	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
7936	17786	28027	1.18	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
8598	18465	28737	3.06	1.0E-118	AA315007.1	EST_HUMAN	EST186814 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
8847	18659	28947	1.75	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8847	18659	28948	1.75	1.0E-118	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
741	10672	20508	0.81	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
1021	12683	20781	1.55	1.0E-119	7705607	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1891	11786	21663	2.09	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3064	12991	22783	1.81	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3202	13126		1.08	1.0E-119	AA916760.1	EST_HUMAN	on10b05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2 CE01214 ;
3870	13781	23573	1.15	1.0E-119	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5111	14979	24753	0.95	1.0E-119	AA077394.1	EST_HUMAN	7B14F03 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14F03
5272	15194	24969	2.45	1.0E-119	AU133399.1	EST_HUMAN	AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
5282	15204	24980	14.93	1.0E-119	M89914.1	NT	Human neurofibromin (NF1) gene, complete cds
5285	15207	24984	3.32	1.0E-119	BE936121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5336	15256	25079	2.24	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDHB03 5'
5726	15633	25736	7.19	1.0E-119	AI150703.1	EST_HUMAN	qb77c09.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
5887	15793	25914	2.79	1.0E-119	X06292.1	NT	Human c-fes/fps proto-oncogene
5895	15801	25925	4.26	1.0E-119	AW974193.1	EST_HUMAN	EST386296 MAGE resequences, MAGM Homo sapiens cDNA
6381	16243	26403	1.42	1.0E-119	BE796614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7883	17733	27977	1.48	1.0E-119	AA465124.1	EST_HUMAN	aa32f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
7998	17848	28089	1.42	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
8535	18407		9.72	1.0E-119	BF569571.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
9348	19671		1.37	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240999-011-f03 CT0212 Homo sapiens cDNA
237	10205	20022	1.4	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
298	10262	20082	1.34	1.0E-120	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
1025	10943	20787	1.67	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1025	10943	20788	1.67	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1406	11311	21172	4.53	1.0E-120	N44873.1	EST_HUMAN	yy40g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273766 5'
1583	11487	21348	3.87	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2060	11950	21847	0.9	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2060	11950	21848	0.9	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2482	12358	22250	0.84	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3267	10262	20082	1.13	1.0E-120	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1), mRNA
4260	14159	23936	1.17	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4260	14159	23937	1.17	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4563	14455	24242	2.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4563	14455	24243	2.79	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5168	15034	24801	0.89	1.0E-120	AI190903.1	EST_HUMAN	qd61f03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733981 3'
5508	15426	25488	13.84	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5508	15426	25489	13.84	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6469	16328	26495	1.49	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
6608	16488	26674	1.67	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
6608	16488	26675	1.67	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
6850	16729	26924	2.44	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183333 5'
6898	16777	26971	2.43	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6898	16777	26972	2.43	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6922	16800	26993	1.33	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
7470	17330	27535	4.54	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
7470	17330	27536	4.54	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
7617	17468	27687	4.72	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
7626	17477	27698	7.31	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
7798	17648	27885	2.53	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
8469	18342	28607	6.4	1.0E-120	BE296387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8914	18722	29013	2.07	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
9495	19111	25288	1.36	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
67	10052	19867	1.04	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
374	10328	20151	0.98	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
707	12674	20465	1.23	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1556	11461	21319	0.99	1.0E-121	AB011163.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
1923	11818	21697	0.89	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1923	11818	21698	0.89	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2055	11945	21841	1.17	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2530	12404	22295	1.05	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2530	12404	22296	1.05	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150286 5'
3042	12969	22763	3.09	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3042	12969	22764	3.09	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3492	13408	23213	1.09	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3492	13408	23214	1.09	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3624	13538	23325	6.61	1.0E-121	AF155156.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4236	14134	23910	1.21	1.0E-121	AI263294.1	EST_HUMAN	qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417 3'
4901	14781	24556	2.55	1.0E-121	X91937.1	NT	H.sapiens ECE-1 gene (exon 17)
5050	14922	24695	1.03	1.0E-121	AI904151.1	EST_HUMAN	CM-BT043-090299-075 BT043 Homo sapiens cDNA
6632	16512	26701	2.58	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
6632	16512	26702	2.58	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8157	18045	28297	4.44	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
8163	18051	28303	2.28	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
8336	18213	28466	4.91	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
8363	18240	28489	3.48	1.0E-121	N69624.1	EST_HUMAN	yv74c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248448 3'
267	10232	20047	3.99	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
333	10292	20107	2.22	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
355	10312	20132	1.54	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
864	10780	20641	2.85	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1201	11111	20957	3.41	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)

Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1667	11569	21435	1.32	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1684	11586	21458	2.01	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1684	11586	21459	2.01	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1772	11671	21549	5.91	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899358 5'
2441	12318	22215	10.56	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2441	12318	22216	10.56	1.0E-122	BF316170.1	EST_HUMAN	601896173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
4738	14623	24409	1.82	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4918	14797		1.2	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BN0-ali-a-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
6051	15337	25390	6.41	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7219	17096	27286	1.35	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9098	18869		4.35	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMM1), mRNA
181	10153	19968	1.07	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
751	10681	20517	1.72	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
751	10681	20518	1.72	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
996	10916	20760	3.79	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1005	10923	20767	5.06	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1218	11126	20976	3.35	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1218	11126	20977	3.35	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1439	11344	21211	1.76	1.0E-123	AJ388641.1	NT	Homo sapiens partial mRNA for immunoglobulin kappa chain variable region (IGVK gene), sample GN02
2052	11942	21837	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2052	11942	21838	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2052	11942	21839	2.98	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2267	12151		4.5	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
5344	15265	25091	1.75	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5344	15265	25092	1.75	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5425	15346	25400	1.29	1.0E-123	BE799746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
5893	15799	25923	2.27	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6186	16071	26221	1.3	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
6509	16368	26545	1.95	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7392	17310	27517	4.14	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7471	17331	27537	12.23	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
8958	18765	29057	5	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
8958	18765	29058	5	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
268	10233	20048	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	10233	20049	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	10239		1.98	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
477	10421	20238	2.11	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
676	10609	20429	2.03	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
676	10609	20430	2.03	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
742	10673	20509	3.67	1.0E-124	AF155654.1	NT	Human putative ribosomal protein S1 mRNA
791	10720	20561	1.06	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
886	10812	20660	1.81	1.0E-124	7705446	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1293	11200	21056	2.59	1.0E-124	11419092	NT	Homo sapiens ring finger protein (RNF), mRNA
1324	11231	21086	5.54	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1324	11231	21087	5.54	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1773	11672	21550	2.35	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noH61 gene)
2016	11907	21797	2.23	1.0E-124	BE879524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
2408	12285	22182	0.85	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3319	13240	23045	0.85	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3446	13363	23169	0.96	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3446	13363	23170	0.96	1.0E-124	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3598	13512	23300	2.95	1.0E-124	X13794.1	NT	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
3825	13737	23528	1.09	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3983	13890	23666	1.19	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4639	14527	24315	1.58	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
4850	14731		1.12	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5039	14911	24685	2.72	1.0E-124	AI204535.1	EST_HUMAN	qf56h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754069 3'
5240	15164	24934	8.97	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5590	15505	25580	6.43	1.0E-124	BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6185	16070	26220	3.31	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene
6805	16684	26874	5.66	1.0E-124	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6930	16808	27002	1.35	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
6930	16808	27003	1.35	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162 O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
7466	17326	27532	2.44	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
7466	17326	27533	2.44	1.0E-124	AV645633.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
7542	17393	27604	7.8	1.0E-124	AI767133.1	EST_HUMAN	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
7542	17393	27605	7.8	1.0E-124	AI767133.1	EST_HUMAN	wi93f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
7676	17526	27752	1.25	1.0E-124	AW503755.1	EST_HUMAN	UI-HF-BN0-akz-b-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078846 5'
8404	18280	28532	2.25	1.0E-124	U94776.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
8645	18509	28788	2.25	1.0E-124	AW665663.1	EST_HUMAN	hj05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'
8767	17916	28162	1.87	1.0E-124	AI446455.1	EST_HUMAN	tj19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN. ;
8767	17916	28163	1.87	1.0E-124	AI446455.1	EST_HUMAN	tj19e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN. ;
9173	10609	20429	3.98	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
9173	10609	20430	3.98	1.0E-124	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
9846	19626	25005	1.99	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9846	19626	25006	1.99	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
316	10278		5.41	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
420	9987	19778	3.92	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
628	10565	20377	1.63	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
628	10565	20378	1.63	1.0E-125	AI110656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
711	10643	20469	1.24	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
842	10769	20619	2.13	1.0E-125	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
982	10905	20750	1.53	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1136	11050	20890	1.63	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1649	12700	21414	1.08	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1769	11668	21545	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1769	11668	21546	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2455	12332	22228	1.15	1.0E-125	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2551	12424	22316	1.65	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
2551	12424	22316	1.65	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INHA) mRNA
2555	12427	22320	2.45	1.0E-125	AI732966.1	EST_HUMAN	oh64d02.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 3'
4450	14344	24136	1.98	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4450	14344	24137	1.98	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4516	14409	24195	0.84	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140798 5'
5581	15496	25573	1.41	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
5612	15527	25610	3.44	1.0E-125	BE892660.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
5965	15870	25993	1.48	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
5965	15870	25994	1.48	1.0E-125	BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689790 5'
6201	15961	26093	6.36	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6201	15961	26094	6.36	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
6974	16851	27043	1.22	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
6974	16851	27044	1.22	1.0E-125	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
7272	17149	27343	4.31	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
7272	17149	27344	4.31	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
8069	17960	28211	3.15	1.0E-125	AF043458.1	NT	Homo sapiens I-REL gene, exon 5
8152	18040	28289	1.86	1.0E-125	AW131202.1	EST_HUMAN	xf59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1] ;
8152	18040	28290	1.86	1.0E-125	AW131202.1	EST_HUMAN	xf59f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2622363 3' similar to TR:Q13284 Q13284 LAMBDA/IOTA PROTEIN KINASE C-INTERACTING PROTEIN. [1] ;
8478	18351	28616	6.13	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
8609	18476	28748	2.92	1.0E-125	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8615	18482	28754	5.15	1.0E-125	AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
8704	18522	28804	2.49	1.0E-125	AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
8793	18607	28896	4.36	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8793	18607	28897	4.36	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8941	18749	29044	1.96	1.0E-125	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
757	10687	20525	0.88	1.0E-126	4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
760	10690	20528	1.2	1.0E-126	M61936.1	NT	Human laminin B1 chain gene, exon 20

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
901	10826	20670	2.03	1.0E-126	X68735.1	NT	H.sapiens gene for alpha1-antichymotrypsin, exon 3
2552	12425	22317	2.24	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3035	12963	22757	6.07	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3035	12963	22758	6.07	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3577	13491	23281	1.21	1.0E-126	X53941.1	NT	H.sapiens DNA for liver cytochrome b5 pseudogene
3605	13519	23307	2.04	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4677	14563	24356	0.96	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4677	14563	24357	0.96	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4728	14614	24400	1.57	1.0E-126	N34078.1	EST_HUMAN	yx78c06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267850 5'
5779	15686	25795	3.68	1.0E-126	AA460075.1	EST_HUMAN	zx66e03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:796444 5' similar to TR:G1145880 G1145880 TITIN ;
5797	15703	25813	3.82	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
5797	15703	25814	3.82	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6660	16540	26737	2.77	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)
8233	18114	28366	1.95	1.0E-126	BF683176.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298240 5'
8806	18620	28910	2.41	1.0E-126	BE261660.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
9635	15098	24890	4.38	1.0E-126	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
165	10138	19954	3.59	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
165	10138	19955	3.59	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19954	2.31	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19955	2.31	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
272	10238	20056	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
272	10238	20057	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
863	10789	20640	1.32	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
898	10823	20669	1.28	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1665	11567	21433	0.98	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2020	11911	21800	1.59	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2020	11911	21801	1.59	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2153	12041	21939	7.45	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2294	12176	22075	4.01	1.0E-127	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2566	12437	22330	2.78	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
2579	12450	22341	0.96	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2579	12450	22342	0.96	1.0E-127	AA450131.1	EST_HUMAN	zx42a02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
3740	13652	23435	0.88	1.0E-127	AW161297.1	EST_HUMAN	au80e08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element ;
4026	13929	23706	1.09	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit IsK mRNA, complete cds
4128	14028	23802	0.86	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4160	14060	23833	21.46	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4160	14060	23834	21.46	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4395	14291	24075	0.92	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4499	14393	24178	4.16	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4532	14425		1.93	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4575	14466	24252	0.98	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5546	15462	25533	3.72	1.0E-127	X85764.1	NT	H.sapiens NOS2 gene, exon 6
5742	15650	25757	2.67	1.0E-127	X84060.1	NT	H.sapiens TCF11 gene, exon 3-6
5816	15722	25835	6.76	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6578	16436	26620	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
6578	16436	26621	1.38	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7558	17409	27624	4.97	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7558	17409	27625	4.97	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7923	17773	28012	1.17	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8498	18371	28634	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
8498	18371	28635	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
8898	18707	29001	2.46	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8898	18707	29002	2.46	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
9397	10138	19954	1.66	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9397	10138	19955	1.66	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9595	19177	25276	2.1	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
452	10396	20214	4.46	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1138	11052	20892	1.48	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1138	11052	20893	1.48	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2025	11916	21805	12.19	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2025	11916	21806	12.19	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2162	12049	21950	13.3	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2395	12273		0.85	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3348	13268	23071	1.13	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4565	14457	24245	5.46	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5865	15771	25890	2.67	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
6140	15988	26123	7.23	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
6976	16853	27046	3.28	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6976	16853	27047	3.28	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7834	17684	27929	1.25	1.0E-128	AA639198.1	EST_HUMAN	ns04a11.r1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS. ;
8092	17983	28232	5.94	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
8101	17991	28240	3.87	1.0E-128	AA926959.1	EST_HUMAN	om68h08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
8230	18111	28364	1.79	1.0E-128	BE384475.1	EST_HUMAN	601277826F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5'
9263	18968		3.66	1.0E-128	AW955290.1	EST_HUMAN	EST367360 MAGE resequences, MAGC Homo sapiens cDNA
116	10353	20182	2.19	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
407	10353	20182	1.35	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1689	11591	21461	2.86	1.0E-129	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1693	11595	21465	2.29	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1693	11595	21466	2.29	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1802	11699	21575	2.43	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2751	12613	22503	1.19	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2751	12613	22504	1.19	1.0E-129	4505682	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3089	13016	22808	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22809	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22810	1.35	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4073	13976	23764	2.2	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4183	14083	23856	9.7	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
4183	14083	23857	9.7	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5

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5706	15614	25715	2.89	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6229	16095	26245	5.17	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6267	16132	26286	7.59	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
6841	16720		3.68	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
8554	18424	28693	3.52	1.0E-129	AA625526.1	EST_HUMAN	af72f07.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'
8618	16132	26286	9.4	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
8888	18699	28993	2.04	1.0E-129	AU143115.1	EST_HUMAN	AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5'
8888	18699	28994	2.04	1.0E-129	AU143115.1	EST_HUMAN	AU143115 Y79AA1 Homo sapiens cDNA clone Y79AA1001410 5'
9250	18960		1.87	1.0E-129	H83155.1	EST_HUMAN	yq49c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199112 5' similar to SP:B48150 B48150 HP-25=HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
9630	19203		1.88	1.0E-129	AL120739.1	EST_HUMAN	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
1643	11547	21408	6.81	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1643	11547	21409	6.81	1.0E-130	BE275192.1	EST_HUMAN	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
1940	11835		2.06	1.0E-130	X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2743	12605		7.7	1.0E-130	AJ010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2849	12777	22564	1.1	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
2849	12777	22565	1.1	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3530	13446	23243	1.07	1.0E-130	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3703	12777	22564	4.77	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3703	12777	22565	4.77	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3857	13768	23560	1.09	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BN0-aky-g-06-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4438	14333	24122	7.48	1.0E-130	AW843993.1	EST_HUMAN	CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5029	14902	24673	1.09	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
5029	14902	24674	1.09	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
6301	16165	26322	2.04	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7119	16996	27187	2.45	1.0E-130	AW956242.1	EST_HUMAN	EST368312 MAGE resequences, MAGD Homo sapiens cDNA
7314	17190	27392	1.57	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
8513	18385	28650	32.43	1.0E-130	M25140.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4
4	9991	19782	2.49	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4	9991	19783	2.49	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
7	9993	19786	1.44	0.0E+00	4885136	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
16	10001	19792	1.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
15	10001	19793	1.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
20	10007	19799	2.45	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
20	10007	19800	2.45	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
24	10011	19804	5.57	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
33	10020	19816	0.97	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
35	10022	19819	2.41	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
51	10038	19845	1.4	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
51	10038	19846	1.4	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
52	10039	19847	1.22	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
52	10039	19848	1.22	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516H08 5'
53	10040	19849	4.14	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
55	10042	19852	8.1	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
55	10042	19853	8.1	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
59	10045	19857	5.8	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
61	10047		2.75	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
69	10054	19869	1.77	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
69	10054	19870	1.77	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19869	1.49	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19870	1.49	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	10058	19875	42.13	0.0E+00	AA953770.1	EST_HUMAN	on89e04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1583870 3' similar to SW:TMOD_HUMAN P28289 TROPOMODULIN. ;
76	10060	19877	1.09	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
77	10061		14.77	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
86	10070	19886	47.55	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
89	10073	19889	13.39	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
94	10079	19895	1.46	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
95	10080	19896	1.03	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
102	10085	19901	6.13	0.0E+00	X91213.1	NT	H.sapiens ncx1 gene (exon 2)
110	10091	19906	1.39	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
111	10091	19906	1.88	0.0E+00	AI623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;

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112	12636	19907	1.83	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
112	12636	19908	1.83	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017 5'
115	10094	19913	0.86	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
126	10100	19921	3.17	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
126	10100	19922	3.17	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
135	10108	19929	1.49	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
135	10108	19930	1.49	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
147	10121		9.05	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
151	10125	19943	2.42	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863803 5'
153	10127		15.84	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
166	10130	19946	1.36	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
158	10132	19947	1.1	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
159	10132	19947	1.18	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
160	10133	19948	2.99	0.0E+00	W73973.1	EST_HUMAN	zd62b05.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
161	10134	19949	1.51	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
164	10137	19952	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
164	10137	19953	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	10145	19960	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
174	10145	19961	4.25	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z CE22631 ;
179	10150	19964	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
179	10150	19965	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
187	10159	19976	130.42	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
192	10164	19981	2.83	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
192	10164	19982	2.83	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
194	10166	19984	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
194	10166	19985	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
203	12661	19991	9.33	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
203	12661	19992	9.33	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
205	10176	19994	1.94	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds

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208	10179		16.66	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
209	10180		3.46	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
215	10186	19999	2.48	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
216	10186	19999	1.95	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
217	10187	20000	1.61	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
224	10195	20004	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
224	10195	20005	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
224	10195	20006	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
225	10195	20004	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
225	10195	20005	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
225	10195	20006	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
226	10195	20004	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
226	10195	20005	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
226	10195	20006	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
238	10206	20023	4.66	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
240	10208		6.54	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
247	10213	20029	3.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
249	10215	20032	1.46	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
257	10223		6.81	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
269	10234	20050	1.14	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	10234	20051	1.14	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
270	10236	20053	2.57	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
281	10246	20066	1.11	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	10246	20067	1.11	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	10247		0.86	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
290	10254	20074	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
290	10254	20075	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
301	10265	20085	4.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
302	10266	20086	3.11	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	12664		5.3	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
304	10267	20087	1.99	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
305	10268		2.03	0.0E+00	AA480002.1	EST_HUMAN	zv18c06.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753994 5'
306	10269	20088	13.28	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
307	10269	20088	9.68	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
311	10273	20092	2.23	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
324	10285	20101	0.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
324	10285	20102	0.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
325	10286	20103	4.18	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
326	10286	20103	2.31	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
341	10300	20115	3.67	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
342	10301	20116	0.86	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
345	10304	20120	3.76	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
348	10307	20125	0.8	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zf31) mRNA, partial cds
353	10311	20129	2.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	10311	20130	2.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	12665	20131	3.4	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	10313	20133	0.89	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
358	10315	20136	1.4	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
359	10316	20137	1.37	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
360	10316	20137	1.52	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
372	10326	20149	1.13	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
381	10365	20188	5.35	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
382	10366	20189	1.01	0.0E+00	AI363014.1	EST_HUMAN	qy81h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54199 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
387	10334	20156	3.43	0.0E+00	AW754180.1	EST_HUMAN	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
390	10336	20159	1.38	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
391	10337	20160	2.04	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
391	10337	20161	2.04	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
392	10338	20162	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
393	10339	20163	1.64	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
393	10339	20164	1.64	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
394	10340	20165	2.43	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
395	10341	20166	0.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	10342	20167	0.84	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
396	10342	20168	0.84	0.0E+00	X74870.1	NT	H.sapiens gene for RNA pol II largest subunit, exons 23-29
400	10346		43.09	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
414	9981	19772	1.31	0.0E+00	R17795.1	EST_HUMAN	yg09a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31652 5'
422	10367		2.61	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
423	10368	20190	2.42	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
424	10369	20191	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
424	10369	20192	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
425	10370	20193	3.51	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
438	10382	20206	2.01	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
443	10387		0.98	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
444	10388		0.91	0.0E+00	BE254447.1	EST_HUMAN	601111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
460	10404	20220	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
460	10404	20221	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
465	10408	20228	1.27	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
465	10408	20229	1.27	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
475	10419	20235	2.26	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	10420	20236	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
476	10420	20237	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
485	10428	20242	2.59	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
487	10430	20244	1.64	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
495	10438	20250	2.17	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
496	12668	20251	1.05	0.0E+00	AW938825.1	EST_HUMAN	PM0-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
498	10440	20253	1.07	0.0E+00	AL117233.1	NT	Novel human gene mapping to chomosome 1
499	10441	20254	1.64	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
508	10450	20263	3.91	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
515	12669	20267	1.97	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
520	10462	20273	1.13	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
526	10468	20280	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
529	10471	20283	11.27	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
530	10472	20284	3.96	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	10472	20285	3.96	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	10477		5.78	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
544	10485	20295	1.79	0.0E+00	AW135324.1	EST_HUMAN	UI-H-BI1-acb-h-04-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
554	10495		3.15	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
571	10510	20318	2.65	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA
584	10522		5.28	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
587	10525	20332	1.73	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
593	10529	20336	1.46	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
598	10534	20342	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
598	10534	20343	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
607	10543	20351	1.38	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
610	10546	20354	0.96	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20355	2.22	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20356	2.22	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20357	0.93	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20358	0.93	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
619	10556	20368	1.34	0.0E+00	AA399486.1	EST_HUMAN	zt60c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
623	10560	20372	6.37	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
627	10564	20375	3.17	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
627	10564	20376	3.17	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
630	10567		3.28	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
637	10574	20388	2.89	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
639	10576	20391	1.06	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
642	10579	20395	1.41	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
646	10583	20398	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
646	10583	20399	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
652	10588	20404	3.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
652	10588	20405	3.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
658	12672		0.95	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
667	10601	20419	4.56	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
672	10606	20423	4.35	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
682	10615	20438	2.03	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
692	10625	20450	19.46	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
696	10629	20454	7.66	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
696	10629	20455	7.66	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
706	10639	20464	1.45	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	10644	20470	3.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	10644	20471	3.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
714	10646	20474	9.78	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
719	10651	20481	1.7	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
739	10670	20505	1.12	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
739	10670	20506	1.12	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	10671	20507	2.4	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
743	10674	20510	1.55	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
743	10674	20511	1.55	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
745	10676	20512	0.78	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
746	10677	20513	1.12	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
747	12676	20514	0.81	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
748	10678	20515	2.17	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
752	10682	20519	3.38	0.0E+00	R48915.1	EST_HUMAN	yj69g08.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154046 5'
753	10683	20520	2.4	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
762	10692	20529	1.58	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
765	10696	20533	2.97	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
775	10705	20544	1.17	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
775	10705	20545	1.17	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
780	10710	20549	2.64	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
784	10714	20553	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	10714	20554	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
789	10718	20560	6.84	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
790	10719		7.06	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
807	10736	20581	1.51	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
808	10737	20582	4.43	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
810	10739	20584	3.91	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
816	10744	20590	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
816	10744	20591	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
821	10749	20596	1.14	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
825	10752	20601	1.55	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	10752	20602	1.55	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
832	10759		1.57	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
836	10763	20613	3.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
836	10763	20614	3.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	10764	20615	7.38	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
838	10765	20616	3.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
839	10766	20617	2.02	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
843	10770	20620	1.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
843	10770	20621	1.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
844	10771	20622	1.97	0.0E+00	AA533272.1	EST_HUMAN	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453
844	10771	20623	1.97	0.0E+00	AA533272.1	EST_HUMAN	nj66d07.s1 NCI_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:997453
845	10772		7.39	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
849	10776	20624	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
849	10776	20625	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	10777	20626	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	10777	20627	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
873	10799	20650	0.87	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
880	10806	20655	1.85	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
880	10806	20656	1.85	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
890	10816	20665	3.93	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
900	10825		7.45	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
903	10825		3.29	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
904	10828	20673	1.5	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
905	10829	20674	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10829	20675	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10829	20676	0.99	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
906	10830	20677	2.14	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds
909	10833	20680	105.13	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
909	10833	20681	105.13	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	10834	20682	167.64	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
910	10834	20683	167.64	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
935	10860	20706	36.3	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
936	10861	20707	13.25	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
937	10862	20708	53.71	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
938	10863	20709	1.9	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
938	10863	20710	1.9	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
946	12681	20717	2.46	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
946	12681	20718	2.46	0.0E+00	AI001948.1	EST_HUMAN	os98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
948	10872	20720	7.21	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
959	10882	20730	2.52	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
967	10890	20736	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
967	10890	20737	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
967	10890	20738	4.64	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
968	10891	20739	1.27	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
968	10891	20740	1.27	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
977	10900	20747	1.25	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
988	10910	20755	1.05	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
989	10911	20756	7.48	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
990	10911	20756	6.69	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
993	10914		1.99	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
994	10914		3.49	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
997	10917	20761	0.84	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
998	10917	20761	1.43	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
999	10917	20761	1.81	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1000	10918	20762	2.23	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1003	10921	20765	2.28	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1007	10925	20769	2.66	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1009	10927		1.94	0.0E+00	AA458680.1	EST_HUMAN	aa86g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRS8_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8 ;

Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1012	10930	20774	1.04	0.0E+00	N43182.1	EST_HUMAN	EST51I24 WATM1 Homo sapiens cDNA clone 51I24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1012	10930	20775	1.04	0.0E+00	N43182.1	EST_HUMAN	EST51I24 WATM1 Homo sapiens cDNA clone 51I24 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1013	10931	20776	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1013	10931	20777	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1017	10935		4.44	0.0E+00	8922933	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1031	10949	20792	2.19	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
1049	10966	20807	1.88	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1049	10966	20808	1.88	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1053	10970	20812	2.52	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1053	10970	20813	2.52	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1054	10971	20814	38.24	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1056	10973		0.93	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1058	10975	20818	3.28	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1066	10982	20827	3.58	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1080	10996	20837	3.6	0.0E+00	BE005208.1	EST_HUMAN	MR0-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA
1103	11019	20861	3.79	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1103	11019	20862	3.79	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1116	11031	20872	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1116	11031	20873	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1117	11032	20874	5.7	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1119	11034	20876	0.86	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1121	11036	20878	10.18	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1123	11038	20879	12.02	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1124	11039	20880	2.03	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1124	11039	20881	2.03	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1128	11042	20884	0.95	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1129	11043	20885	1	0.0E+00	AI147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'
1131	11045	20887	1.44	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1140	11054	20896	1.13	0.0E+00	9966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1152	11065	20908	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	11065	20909	2.31	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1154	11067	20911	1.59	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1161	11074	20920	1.02	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1191	11101		1.13	0.0E+00	7657336	NT	Homo sapiens mutL (E. coli) homolog 3 (MLH3), mRNA
1206	11116	20962	1.14	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1206	11116	20963	1.14	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1207	11117	20964	1.31	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1208	12687	20965	0.95	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1226	11134	20988	3.62	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1227	11135	20989	1.3	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1245	11152		1.48	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1253	11160	21009	45.69	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1260	11167	21018	3.66	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1266	11173	21022	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1266	11173	21023	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1278	11186	21036	6.42	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1278	11186	21037	6.42	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1278	11186	21038	6.42	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1279	11187		2.6	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1289	12689	21050	1.1	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1289	12689	21051	1.1	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1295	11202	21057	1.71	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1296	11203	21058	0.82	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1298	11205	21059	1.07	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1300	11207	21061	4.1	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1301	11208	21062	1.06	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1302	11209	21063	4.64	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1303	11210	21064	4.1	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1303	11210	21065	4.1	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1315	11221	21078	1.35	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1386	11291	21147	0.89	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyld gene
1393	11298	21156	9.13	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1396	11301	21160	0.96	0.0E+00	AI208756.1	EST_HUMAN	qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5 CE14213 ;
1397	11302	21161	8.18	0.0E+00	6042206	NT	RAN, member RAS oncogene familyHomo sapiens RAN, member RAS oncogene family (RAN), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1407	11312	21173	1.4	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1407	11312	21174	1.4	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1409	11314	21177	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1409	11314	21178	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1412	11317	21180	5.25	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1421	11327	21192	3.51	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1432	11337	21203	9.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1432	11337	21204	9.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1437	11342	21208	1.02	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1437	11342	21209	1.02	0.0E+00	U35637.1	NT	Human nebulin mRNA, partial cds
1446	11350	21214	3.05	0.0E+00	AL132999.1	NT	Novel human gene on chromosome 20
1447	11352	21215	1.03	0.0E+00	AL137764.1	NT	Novel human gene mapping to chomosome 1
1451	11356	21220	1.22	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	11359	21223	4.97	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1456	11361	21225	1.51	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	11361	21226	1.51	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1457	11362		0.97	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1462	11367	21231	3.65	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1462	11367	21232	3.65	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1495	11399	21259	1.32	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1509	11414	21273	0.95	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116 5'
1515	11420	21276	11.95	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1515	11420	21277	11.95	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1517	11422	21280	0.97	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1519	11424		2.03	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1520	11425	21283	3.9	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1520	11425	21284	3.9	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1521	11426	21285	3.12	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1522	11427		8.41	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1527	11432	21289	5.02	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1530	11435	21291	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1530	11435	21292	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1531	12697		10.12	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1532	11436	21293	11.11	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1541	11446	21306	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1541	11446	21307	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1543	11448	21308	12.91	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1562	11467	21325	1.66	0.0E+00	Z83738.1	NT	H.sapiens hH2B/e gene
1563	11468	21326	1.38	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1563	11468	21327	1.38	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1564	11469	21328	5.5	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1564	11469	21329	5.5	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1566	12698	21330	1.5	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1570	11474	21331	0.98	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1572	11476	21334	2.49	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1572	11476	21335	2.49	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1574	11478	21336	14.05	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1574	11478	21337	14.05	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1576	11480	21339	0.94	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1591	11495	21355	4.67	0.0E+00	H26973.1	EST_HUMAN	yo76c05.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1602	11507	21368	1.4	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1602	11507	21369	1.4	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1645	11549	21410	1.27	0.0E+00	AI768104.1	EST_HUMAN	wg81b07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1646	11550	21411	3.33	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1650	11553	21415	1.56	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	11553	21416	1.56	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1652	11555	21418	1.22	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1653	11556	21419	0.92	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1657	11559	21423	1.11	0.0E+00	4557610	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1659	11561	21426	2.99	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1659	11561	21427	2.99	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1661	11563	21429	1.21	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1661	11563	21430	1.21	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
1664	11566		7.85	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1672	11574	21442	4.55	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1677	11579	21448	1.02	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1677	11579	21449	1.02	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1680	11582	21453	1.43	0.0E+00	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1685	11587	21460	2.59	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1687	11589		2.6	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1699	12702	21472	0.87	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1710	11611	21481	1.75	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1745	12703		13.81	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1749	11649	21517	0.9	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1749	11649	21518	0.9	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1751	11651	21521	1.23	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1754	11654		1.13	0.0E+00	W76571.1	EST_HUMAN	zd66g09.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:345664 5'
1755	12704	21525	3.89	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1765	11664	21538	7.25	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1767	11666	21541	4.6	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1768	11667	21542	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1768	11667	21543	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1768	11667	21544	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1781	11680	21558	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products
1781	11680	21559	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobin superfamily, member 3 (IGSF3) mRNA, and translated products
1793	11691	21566	10.22	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1793	11691	21567	10.22	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1804	11701	21576	3.19	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1804	11701	21577	3.19	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1805	11702	21578	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1805	11702	21579	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1809	11706	21584	1.47	0.0E+00	AW207280.1	EST_HUMAN	UI-H-BI1-afn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1809	11706	21585	1.47	0.0E+00	AW207280.1	EST_HUMAN	UI-H-BI1-afn-f-07-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'

Table 4
Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1832	11729	21603	2.08	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1832	11729	21604	2.08	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1852	11748	21623	0.99	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1881	11777	21651	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1881	11777	21652	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1889	11785		1.65	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1890	12707	21661	4.06	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1890	12707	21662	4.06	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1895	11790	21669	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1895	11790	21670	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1898	11794		5.25	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1903	11799		1.9	0.0E+00	M65632.1	NT	Human topoisomerase I pseudogene 1
1905	12708	21678	0.94	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1913	11808	21685	1.97	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1913	11808	21686	1.97	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1924	11819		1.12	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
1926	11821	21700	1.15	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1926	11821	21701	1.15	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1927	11822	21702	8.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1927	11822	21703	8.13	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1937	11832	21715	1.21	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1937	11832	21716	1.21	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1943	11838	21720	2.01	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1943	11838	21721	2.01	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1945	11840	21722	1.33	0.0E+00	AW193024.1	EST_HUMAN	xl69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
1945	11840	21723	1.33	0.0E+00	AW193024.1	EST_HUMAN	xl69b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
1946	11841	21724	8.4	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1946	11841	21725	8.4	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1948	11843	21727	0.92	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
1948	11843	21728	0.92	0.0E+00	Z47556.1	NT	H.sapiens genes for semenogelin I and semenogelin II
1955	11850	21737	2.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1975	11868	21759	0.86	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1975	11868	21760	0.86	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2011	11903	21793	1.09	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2011	11903	21794	1.09	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2013	11905	21795	0.96	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2014	11906	21796	5.46	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2015	11314	21177	1.01	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2016	11314	21178	1.01	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2017	11908	21798	1.95	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2017	11908	21799	1.95	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2019	11910		2.34	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2021	11912		1.6	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2022	11913	21802	0.92	0.0E+00	Z42399.1	EST_HUMAN	HSC0IC021 normalized infant brain cDNA Homo sapiens cDNA clone c-0ic02
2024	11915		1.94	0.0E+00	AI244247.1	EST_HUMAN	qv90f08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element;
2029	11920	21811	2.59	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2031	11922	21813	1.5	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2031	11922	21814	1.5	0.0E+00	BF315325.1	EST_HUMAN	601902604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2035	11926	21819	2.42	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2035	11926	21820	2.42	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2040	11931	21826	2.53	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comlete cds
2040	11931	21827	2.53	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, comlete cds
2045	11936	21831	1.32	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2067	11957		2.63	0.0E+00	BE767964.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2068	11958		1.13	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds
2070	11960	21854	3.09	0.0E+00	BF027562.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2071	11961	21855	2	0.0E+00	4503756	NT	Homo sapiens flavin containing monooxygenase 2 (FMO2) mRNA
2073	11963	21856	0.99	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2074	11964	21857	1.16	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2076	11966	21859	1.96	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2076	11966	21860	1.96	0.0E+00	AI904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2112	12001		1.19	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2132	12020		1.6	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3'end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2138	12026	21922	1.02	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2140	12028	21925	1.09	0.0E+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2141	12029	21926	10.46	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2141	12029	21927	10.46	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2143	12031	21929	1.4	0.0E+00	AA931691.1	EST_HUMAN	oo32e01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2145	12033		0.9	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
2148	12036	21933	17.1	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150734 5'
2149	12037	21934	11.29	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2152	12040	21937	2.35	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2152	12040	21938	2.35	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2156	12714	21943	1.77	0.0E+00	BF313617.1	EST_HUMAN	601900261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129622 5'
2159	12046	21946	1.92	0.0E+00	BE018750.1	EST_HUMAN	bb84e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;
2160	12047	21947	0.92	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2160	12047	21948	0.92	0.0E+00	AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2168	12055	21956	2.32	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2168	12055	21957	2.32	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2169	12056	21958	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2169	12056	21959	2.63	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2174	12061		1.04	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2193	12080	21984	7.56	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2199	12086	21988	1.44	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2206	12093	21996	1.09	0.0E+00	BE895281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2209	12096	21999	0.87	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2209	12096	22000	0.87	0.0E+00	BE905563.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2212	12098	22002	1.36	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2253	12137	22034	4.16	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2253	12137	22035	4.16	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2254	12138	22036	2.51	0.0E+00	AI076404.1	EST_HUMAN	oz09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2256	12140	22038	2.21	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2256	12140	22039	2.21	0.0E+00	AA429001.1	EST_HUMAN	zv78a11.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2258	12142	22041	2.23	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2263	12147	22047	1.19	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2264	12148	22048	2.03	0.0E+00	6325466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2271	12155	22054	1	0.0E+00	BE676095.1	EST_HUMAN	7f22a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939 KIAA0857 PROTEIN ;
2274	12158	22056	10.08	0.0E+00	AF044571.1	NT	Homo sapiens phosphorylase kinase alpha subunit (PHKA2) gene, exon 32
2275	12159	22057	2.72	0.0E+00	AI625542.1	EST_HUMAN	ty57c08.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2283182 3'
2280	12164	22061	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2280	12164	22062	1.76	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2291	12173	22072	4.26	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2291	12173	22073	4.26	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
2300	12182	22079	2.88	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2304	12185	22083	1.75	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2305	12186		5.71	0.0E+00	BE794026.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2306	12187	22084	0.98	0.0E+00	AW867076.1	EST_HUMAN	MR1-SN0033-120400-002-a04 SN0033 Homo sapiens cDNA
2307	12188	22085	1.97	0.0E+00	7662017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2308	12189	22086	1.44	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2308	12189	22087	1.44	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2309	12190		2.31	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2310	12191	22088	7.57	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2310	12191	22089	7.57	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2310	12191	22090	7.57	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	12208		0.96	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2363	12243	22138	1.34	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2366	12246		3.64	0.0E+00	AI042035.1	EST_HUMAN	ox60b02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662 O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ;
2369	12249	22141	0.98	0.0E+00	AW303998.1	EST_HUMAN	xv15f07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924 O54924 EXO84. ;
2371	12251		2.03	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2382	12262		1.69	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2386	12265	22158	5.63	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2390	12268	22162	2.48	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2390	12268	22163	2.48	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2398	12276	22172	2.28	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2402	12279	22176	0.98	0.0E+00	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
2410	12287	22185	3.95	0.0E+00	5729777	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2414	12291	22188	0.87	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2414	12291	22189	0.87	0.0E+00	BE831003.1	EST_HUMAN	CM0-MT0033-150600-428-h11 MT0033 Homo sapiens cDNA
2419	12296	22193	2.27	0.0E+00	BF569144.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2428	12305	22201	2.66	0.0E+00	AW466922.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2430	12307	22202	3.45	0.0E+00	AW501010.1	EST_HUMAN	UI-HF-BP0p-ais-c-07-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2444	12321	22219	2.08	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2444	12321	22220	2.08	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2457	12334		2.35	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2462	12339	22233	16.13	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2463	11792	21671	1.18	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2464	12340	22234	1.8	0.0E+00	BF509482.1	EST_HUMAN	UI-H-BI4-aoz-b-08-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2467	12343	22236	2.25	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2469	12345		5.57	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2471	12347	22239	1.99	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2472	12348	22240	1.96	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2473	12349	22241	55.78	0.0E+00	BE150865.1	EST_HUMAN	RC4-HT0276-160200-013-d05 HT0276 Homo sapiens cDNA
2474	12350	22242	1.14	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2475	12351	22243	3.21	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2481	12357	22249	1.64	0.0E+00	BE886490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2486	12361	22255	4.39	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2486	12361	22256	4.39	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2488	12363	22259	0.97	0.0E+00	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2504	12379	22267	1.27	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2509	12383	22274	3.8	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2509	12383	22275	3.8	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2510	12384	22276	1.19	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2510	12384	22277	1.19	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2511	12385	22278	0.99	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:O00246 O00246 HYPOTHETICAL 9.3 KD PROTEIN ;
2514	12388	22280	7.65	0.0E+00	AF245505.1	NT	Homo sapiens adlican mRNA, complete cds
2540	12414	22304	1.05	0.0E+00	BE296613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2553	12654	22318	2.37	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2553	12654	22319	2.37	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12426		3.85	0.0E+00	BF513835.1	EST_HUMAN	UI-H-BW1-amp-f-12-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2560	12432	22325	2.8	0.0E+00	BF672818.1	EST_HUMAN	602152653F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293612 5'
2562	12434		1.16	0.0E+00	BE616695.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'
2569	12440	22332	1.34	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2570	12441	22333	0.97	0.0E+00	AI571737.1	EST_HUMAN	tn19b08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb:L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2571	12442	22334	2.27	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) mRNA
2573	12444	22336	5.78	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2574	12445	22337	1.03	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2574	12445	22338	1.03	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2577	12448	22339	1.1	0.0E+00	BE293328.1	EST_HUMAN	601143722F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3051389 5'
2585	12456		10.42	0.0E+00	BE792472.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2595	12465	22358	2.46	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2601	12727	22365	7.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
2608	12476		1.09	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2609	12477	22369	5.19	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2613	12481	22370	1.17	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2616	12484	22373	0.98	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001984 5'
2617	12485	22374	1.41	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2619	12487	22376	1.21	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2619	12487	22377	1.21	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2622	12490	22380	1.29	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2626	12494	22385	1	0.0E+00	BF000018.1	EST_HUMAN	7h15h05.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'
2627	12495	22386	3.25	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2628	12496		2.74	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2656	12523	22413	1.74	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2690	12555		8.72	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (matastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2691	12556	22443	0.88	0.0E+00	BE794884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2698	12562	22452	3.59	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2700	12564	22454	1.08	0.0E+00	7669517	NT	Homo sapiens neuregulin 1 (NRG1),transcript variant SMDF, mRNA
2701	12565	22455	10.23	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2708	12571	22462	10.37	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2709	12572	22463	3.2	0.0E+00	BF680632.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2712	12731	22467	13.51	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2713	12575		1.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2715	12577	22470	2.17	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2715	12577	22471	2.17	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2716	12578	22472	0.9	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2716	12578	22473	0.9	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2717	12579	22474	2.2	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2718	12580		15.67	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLCCLD07 3'
2719	12581	22475	1.72	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2719	12581	22476	1.72	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2723	12585	22479	3.21	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2723	12585	22480	3.21	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2727	12589	22485	2.2	0.0E+00	BE747193.1	EST_HUMAN	601580903F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929472 5'
2730	12592	22488	0.97	0.0E+00	BE176836.1	EST_HUMAN	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA
2741	12603		1.3	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2742	12604	22498	3.47	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-amw-e-07-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2748	12610		1.07	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2754	12616	22507	4.95	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2758	12620	22513	1.73	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2761	12623	22515	9.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2761	12623	22516	9.56	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2763	12625		11.15	0.0E+00	AI879163.1	EST_HUMAN	au55d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2766	12628	22521	1.97	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214679 5'
2767	12629	22522	2.91	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2769	12631	22523	1.11	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2769	12631	22524	1.11	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2770	12632	22525	10.1	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2770	12632	22526	10.1	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2775	10151	19966	4.6	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3068 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2778	12638		1.94	0.0E+00	AB033281.1	NT	Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2784	10649	20479	1.37	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2784	10649	20480	1.37	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2789	10941	20784	3.58	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	10941	20785	3.58	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2805	12735	22534	2.39	0.0E+00	X85980.1	NT	H.sapiens serine hydroxymethyltransferase pseudogene
2806	12736		1.27	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2808	12738		1.1	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2814	12743		1.07	0.0E+00	AJ238852.1	NT	Homo sapiens partial rpl3 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes
2815	12744	22538	2.24	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2819	12748	22541	5.94	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
2822	12751	22543	1.58	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2822	12751	22544	1.58	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281299-003-e02 HT0343 Homo sapiens cDNA
2824	12753		1.38	0.0E+00	X73428.1	NT	H.sapiens Id3 gene for HLH type transcription factor
2826	12755		2.84	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2828	12757	22547	2.58	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2833	12761	22551	43.46	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
2833	12761	22552	43.46	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
2837	12765	22555	1.34	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2838	12766		4.62	0.0E+00	Y10658.1	NT	H.sapiens mRNA for nuclear DNA helicase II
2839	12767		0.96	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2840	12768	22556	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2840	12768	22557	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2851	12779	22568	2.42	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2854	12782	22572	1.35	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2855	12783	22573	1.25	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2855	12783	22574	1.25	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2856	12784		3.42	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2858	12786	22576	4.95	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2858	12786	22577	4.95	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2866	12794	22588	1.64	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2866	12794	22589	1.64	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2867	12795	22590	1.08	0.0E+00	AA215579.1	EST_HUMAN	zr96b11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2874	12801		3.09	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2877	12804	22599	1.16	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2878	12805	22600	18.66	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2879	12806	22601	1.25	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN. ;
2879	12806	22602	1.25	0.0E+00	AI561002.1	EST_HUMAN	tn18d07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN. ;
2881	12808	22604	1.87	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2882	12809	22605	1.5	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2897	12824	22617	1.34	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2897	12824	22618	1.34	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2898	12825	22619	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2898	12825	22620	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2901	12828	22623	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2901	12828	22624	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2902	12829	22625	3.23	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2902	12829	22626	3.23	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2907	12833	22630	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN. ;
2907	12833	22631	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1 Q9VLN1 CG17293 PROTEIN. ;
2915	12842	22642	2.03	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2915	12842	22643	2.03	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2917	12844	22645	0.94	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2917	12844	22646	0.94	0.0E+00	4885214	NT	Homo sapiens v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2924	12851	22651	1.6	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
2927	12854	22654	1.3	0.0E+00	X15309.1	NT	H.sapiens NF-H gene, exon 4
2927	12854	22655	1.3	0.0E+00	X15309.1	NT	H.sapiens NF-H gene, exon 4
2929	12856	22657	7.93	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
2943	12870		1.13	0.0E+00	AI149880.1	EST_HUMAN	qf43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
2952	12879	22677	0.84	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2952	12879	22678	0.84	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
2953	12880	22679	0.97	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
2954	12881	22680	2.15	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2964	12891	22689	1.33	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2965	12892	22690	1.59	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2965	12892	22691	1.59	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2990	12918		0.89	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2992	12920	22714	1.04	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3001	12929	22721	0.82	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3006	12934		4.85	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3009	12937	22730	7.86	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3009	12937	22731	7.86	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3011	12939		5.08	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3014	12942	22735	2.02	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3017	12945		1.74	0.0E+00	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a>
3019	12947	22739	0.99	0.0E+00	4504664	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3038	12966	22760	2.79	0.0E+00	X03529.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3043	12970		1.85	0.0E+00	AF199355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3047	12974	22767	1.89	0.0E+00	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3068	12995	22786	2.85	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3069	12996	22787	3.97	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3074	13001	22791	4.21	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3075	13002	22792	1.64	0.0E+00	AF042076.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3102	13028	22824	3.45	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3111	13036	22832	19.64	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3115	13040	22836	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3115	13040	22837	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3123	13048	22845	9.41	0.0E+00	T94870.1	EST_HUMAN	ye32f03.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3138	13063	22862	1.1	0.0E+00	BF243336.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3140	13065	22863	1.03	0.0E+00	AI968086.1	EST_HUMAN	wu12h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2516803 3'
3145	13070	22870	3.99	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3145	13070	22871	3.99	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3156	13081	22883	1.5	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3156	13081	22884	1.5	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
3163	13088	22892	7.73	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3164	13089	22893	3.26	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3164	13089	22894	3.26	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3180	13105	22910	2.44	0.0E+00	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3183	13108	22912	2.23	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3188	13113	22918	0.82	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3188	13113	22919	0.82	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3190	13115	22920	26.3	0.0E+00	AA774783.1	EST_HUMAN	ae87b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3198	13123	22928	4.53	0.0E+00	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3198	13123	22929	4.53	0.0E+00	AF286598.1	NT	Homo sapiens angiostatin binding protein 1 mRNA, complete cds
3210	13134	22935	1.56	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3215	13139	22942	3.35	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3224	13148		4.39	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3225	13149	22949	1.19	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3227	13151	22951	4.15	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3237	15066	22959	3.46	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3237	15066	22960	3.46	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3252	13175	22973	2	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3253	13176	22974	0.89	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3282	13203	23003	4.86	0.0E+00	AI589294.1	EST_HUMAN	tr58f08.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11. ;contains Alu repetitive element;
3289	13211	23011	2.98	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3289	13211	23012	2.98	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3290	13212	23013	1	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3290	13212	23014	1	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3292	13214	23015	1.01	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3292	13214	23016	1.01	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3296	13218	23019	11.07	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3298	13220	23021	0.96	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3303	13224	23026	0.99	0.0E+00	BE779039.1	EST_HUMAN	601464995F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
3350	13270	23073	3.01	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3357	13276	23076	1.66	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3357	13276	23077	1.66	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3360	13279	23079	1.43	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3361	13280	23080	0.99	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1l-a isoform (CACNA1I) mRNA, complete cds
3377	13295	23094	1.35	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3377	13295	23095	1.35	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3378	13296	23096	0.96	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3381	13299	23098	1.71	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3390	12565	22455	6.04	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3395	13312	23111	2.08	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3398	13315	23115	1.53	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3398	13315	23116	1.63	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3400	13317	23118	5.53	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC incompatibility determinants
3402	13319	23120	1.21	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3409	13326	23126	3.68	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3409	13326	23127	3.68	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE. ;
3413	13330	23132	2.67	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3420	13337	23141	2.86	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3420	13337	23142	2.86	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3426	13343	23148	1.14	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3431	13348	23153	6.18	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3436	13353	23157	1.01	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3436	13353	23158	1.01	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3440	13357	23163	2.06	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3440	13357	23164	2.06	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3448	13365	23172	1.23	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3455	13371	23175	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	13371	23176	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3455	13371	23177	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab51f12.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3458	13374	23180	1.11	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3461	13377	23182	2.23	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3461	13377	23183	2.23	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3463	13379	23185	1.43	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3470	13386	23191	0.92	0.0E+00	AI384007.1	EST_HUMAN	te35g12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498 O00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3473	13389	23194	0.96	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3495	13412	23217	0.82	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3497	13414		1.3	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3505	13422	23225	1.39	0.0E+00	AL133204.1	NT	Novel human gene mapping to chomosome X
3507	13423	23226	0.96	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3527	13443		0.98	0.0E+00	AI081907.1	EST_HUMAN	ox77c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T19B4.4 CE13742 ;
3529	13445	23242	1.26	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3533	13449		4.53	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3540	13456		0.95	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3541	13457	23250	7.43	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3564	13478		1.1	0.0E+00	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3566	13480	23269	0.98	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3566	13480	23270	0.98	0.0E+00	AW664693.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3569	13483	23274	1.13	0.0E+00	4826763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3571	13486	23277	0.98	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3578	13492	23282	0.79	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3578	13492	23283	0.79	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3596	13510	23297	1.51	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3600	13514		28.67	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3616	13530	23316	4.26	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3619	13533	23318	3.26	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3619	13533	23319	3.26	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3623	13537	23323	1.5	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3623	13537	23324	1.5	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3626	13540	23326	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3626	13540	23327	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3630	13544	23331	1.79	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3632	13546	23333	1.25	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, *partial cds*
3645	13559	23344	3.53	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3645	13559	23345	3.53	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-ajs-e-12-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3668	13582	23369	0.99	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3669	13583	23370	1.03	0.0E+00	AA463659.1	EST_HUMAN	aa06g01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4. [1] ;
3677	13591	23377	3.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3687	13600	23387	0.91	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3699	13613	23397	3.88	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3701	13615	23399	7.88	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3705	13618	23401	1.02	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3705	13618	23402	1.02	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3746	13659	23441	1.13	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3747	13660		1.01	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3748	13661	23442	2.3	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3751	13664	23446	1.69	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3751	13664	23447	1.69	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3752	13665	23448	1.45	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3756	13669	23453	1.1	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3758	13671	23455	1.1	0.0E+00	AI377699.1	EST_HUMAN	te62f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3759	13672		1.7	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3760	13673	23456	4.46	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
3763	13676	23458	11.67	0.0E+00	S78685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/BIR1) gene, complete cds
3764	13677	23459	2	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3765	13678	23460	2.39	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3768	13681	23462	1.31	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3768	13681	23463	1.31	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3769	13682	23464	1.97	0.0E+00	4504534	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1D (HTR1D) mRNA
3773	13685	23467	1.61	0.0E+00	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3775	13687	23470	1.12	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3780	13692	23478	5.67	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3780	13692	23479	5.67	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3782	13694	23482	3.93	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3784	13696	23483	1.63	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3787	13699	23486	0.99	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3788	13700	23487	1.87	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3790	13702	23489	0.82	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3799	13711	23498	2.54	0.0E+00	AI864727.1	EST_HUMAN	wk01f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR:O43340 O43340 R28830_2. ;contains element PTR7 repetitive element ;
3802	13714	23502	6.08	0.0E+00	4506742	NT	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3807	13719	23508	1.41	0.0E+00	AL040338.1	EST_HUMAN	DKFZp434N0413_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0413 5'
3813	13725	23515	1	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3813	13725	23516	1	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3815	13727	23518	2.45	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3816	13728		1.8	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3820	13732	23521	0.87	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3830	13742	23534	1.27	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3833	13745	23537	1.62	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3840	13751	23544	1.75	0.0E+00	BF356295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
3842	13753	23546	1.4	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
3842	13753	23547	1.4	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1996726 similar to MXRA5 Matrix remodeling associated gene 5
3848	13759	23552	1.78	0.0E+00	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
3853	13764	23557	3.2	0.0E+00	BE378602.1	EST_HUMAN	601236966F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
3854	13765	23558	1.27	0.0E+00	BE313146.1	EST_HUMAN	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509743 5'
3860	13771	23563	0.97	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100100-003-h09 LT0031 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
3893	13803	23587	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3893	13803	23588	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3903	13813		3.93	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3905	13815		5.44	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3912	13822	23603	1.53	0.0E+00	AL118494.1	NT	Novel human gene mapping to chomosome 20
3916	13825	23605	2.89	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3924	13833	23613	1.46	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
3935	13844		25.75	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3939	13847	23623	1.18	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3940	13848	23624	2.05	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
3960	13867	23645	6.24	0.0E+00	AB015610.1	NT	Chlorocebus aethiops mRNA for ribosomal protein S4X, complete cds
3968	13875		3.79	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
3976	13883	23658	3.28	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3976	13883	23659	3.28	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3981	13888	23663	5.63	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3981	13888	23664	5.63	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
3993	13900	23677	0.81	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART) mRNA
4000	13906	23682	4.89	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4001	13907	23683	1.94	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4003	13909	23684	1.28	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4004	13910	23685	6.1	0.0E+00	11419297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4005	13911	23686	1.58	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4013	13919	23695	2.7	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4017	15071	23697	0.85	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4022	11031	20872	0.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4022	11031	20873	0.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4028	13931	23707	0.99	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4029	13932	23708	1.16	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4029	13932	23709	1.16	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4032	13935	23711	1.05	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4032	13935	23712	1.05	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4041	13944	23722	4.59	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'
4041	13944	23723	4.59	0.0E+00	AI982597.1	EST_HUMAN	wu04d04.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4044	13946	23725	0.88	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4044	13946	23726	0.88	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4048	13950		1.99	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'
4055	13957	23733	0.97	0.0E+00	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4056	13958	23734	1.98	0.0E+00	5729725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4064	13966		6.19	0.0E+00	AW675599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:THI2_BOVIN Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4069	13971	23748	1.52	0.0E+00	AW408788.1	EST_HUMAN	UI-HF-BM0-adx-c-02-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4071	13973	23751	1.33	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4071	13973	23752	1.33	0.0E+00	8922466	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4081	13983		1.96	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4098	13998	23775	7.82	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4098	13998	23776	7.82	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element;contains element MER35 repetitive element ;
4113	14013	23791	3.79	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4113	14013	23792	3.79	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4126	14026	23801	0.87	0.0E+00	4506882	NT	Homo sapiens semenogelin I (SEMG1) mRNA
4130	14030	23803	8.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4130	14030	23804	8.21	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4137	14037		0.88	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4163	14063	23837	1.13	0.0E+00	AJ003145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4176	14076	23851	7.84	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds
4190	14090	23868	0.95	0.0E+00	AW936689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4196	14096	23876	0.88	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4196	14096	23877	0.88	0.0E+00	4826827	NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4198	14098	23879	5.73	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds
4206	14105		1.92	0.0E+00	AI189844.1	EST_HUMAN	qd23f06.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20.b2 MER20 repetitive element ;
4210	14108		4.09	0.0E+00	U14520.1	NT	Human CBFA3 (Cbfa3) gene, partial cds
4224	14122	23897	0.98	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4230	14128	23904	0.87	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4230	14128	23905	0.87	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4237	14135	23911	1.17	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4237	14135	23912	1.17	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4245	14144	23917	10.2	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4263	14162		1.15	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4268	14167	23943	1.59	0.0E+00	U03901.1	NT	Human Ig light chain VL1 region germline (humlv1c2c) gene, partial cds
4274	14173	23950	5.17	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4278	14177	23955	2.78	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4278	14177	23956	2.78	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4284	14183	23962	1.58	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4284	14183	23963	1.58	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4289	14187	23969	8.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4289	14187	23970	8.95	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4299	14197	23982	10.81	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4302	14200	23984	0.98	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4333	14230	24012	1.1	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4341	14238		5.85	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4346	14243	24025	8.1	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4346	14243	24026	8.1	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4368	14264		1.92	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
4401	14296	24080	40.23	0.0E+00	AW084964.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q09666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4403	15073		1.91	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4405	14299	24083	1.38	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4408	14302		7.5	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4410	14304	24087	1.29	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101199-002-d03 HT0305 Homo sapiens cDNA
4416	14310	24094	1.83	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4416	14310	24095	1.83	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4418	14312	24097	3.91	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4419	14313	24098	2.3	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4424	14318	24104	1.47	0.0E+00	Z66526.1	NT	H.sapiens pancreatic polypeptide receptor PP1 gene
4429	14324	24111	1.12	0.0E+00	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4430	14325	24112	1.95	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	14325	24113	1.95	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4439	15074	24123	3.08	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4444	14338	24128	5.37	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4449	14343	24135	1.92	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4452	14346	24139	1.36	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4462	14356	24147	15.15	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4473	14367	24156	1.47	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4477	14371	24161	1.58	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4481	14375		2.78	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4483	14377	24163	9.78	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4483	14377	24164	9.78	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4498	14392	24177	2.04	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4500	14394	24179	8.67	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4500	14394	24180	8.67	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4511	14404		0.84	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4523	14416		1.5	0.0E+00	AA174072.1	EST_HUMAN	zp18g08.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4526	14419		1.55	0.0E+00	7657410	NT	Homo sapiens odz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4528	14421		1.22	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4529	14422	24205	1.71	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4530	14423	24206	4.37	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4531	14424		1.89	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4541	14434	24216	1.91	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4541	14434	24217	1.91	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4542	14435	24218	1.3	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4542	14435	24219	1.3	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4543	14436	24220	1.18	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4554	14013	23791	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4554	14013	23792	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4560	14452	24238	21.96	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4566	14458	24246	2.32	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4574	14465		2.01	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4580	14470	24257	2.65	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4580	14470	24258	2.65	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4581	14471	24259	2.55	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4585	14474	24262	1.82	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4585	14474	24263	1.82	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4586	10108	19929	1.03	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4586	10108	19930	1.03	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4587	14475		0.99	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4593	14481	24267	1.11	0.0E+00	BE390050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607067 5'
4614	14502	24290	37.36	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
4617	14505	24293	3.14	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4617	14505	24294	3.14	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4620	14508	24297	1.12	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4621	14509	24298	1.34	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4636	14524		1.54	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4644	14532	24319	0.95	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4644	14532	24320	0.95	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4652	14538	24327	1.09	0.0E+00	AF026801.1	NT.	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26
4655	14541	24330	0.92	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4655	14541	24331	0.92	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4676	14562	24355	1.78	0.0E+00	AW444637.1	EST_HUMAN	UI-H-BI3-ajw-c-04-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
4681	14567	24363	1.11	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4686	14572		1.8	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4697	14583		2.04	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4735	14620		2.83	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4737	14622	24408	2.79	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4739	14624	24410	1.3	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4740	14625	24411	1.47	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4741	14626	24412	3.51	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4743	14628	24414	61.82	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4744	14629	24416	1.4	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4746	14631	24417	0.97	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4748	14633	24419	0.8	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4752	14637	24424	7.78	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4756	14641	24428	0.95	0.0E+00	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4757	14642	24429	1.66	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4757	14642	24430	1.66	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4759	14644	24432	1.69	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4759	14644	24433	1.69	0.0E+00	X94628.1	NT	H.sapiens MeCP-2 gene
4762	14647	24436	1.08	0.0E+00	M55582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4763	14648	24437	3.22	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4776	14660	24447	0.99	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2I) mRNA
4786	14671	24458	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4788	14673	24460	1.44	0.0E+00	X92841.1	NT	H.sapiens MICA gene
4791	14676	24463	1.97	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4792	14677	24464	1.18	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4794	14679	24466	2.26	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4795	14680	24467	1.05	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
4797	14682	24469	8.64	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4799	14684	24471	1.2	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4800	14685	24472	1.61	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA
4801	14686		1.33	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RhD, therad 7
4806	14690	24477	24.91	0.0E+00	AF055066.1	NT	Homo sapiens MHC class 1 region
4808	14692		2.43	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
4809	14693	24480	2.46	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4812	14013	23791	5.48	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4812	14013	23792	5.48	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4814	14697	24484	0.86	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4824	14708	24490	12.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4827	14709	24493	0.95	0.0E+00	D63562.1	NT	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 44 and partial cds

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4831	14713	24496	1.52	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) (FDPS) mRNA
4837	14319	24105	1.06	0.0E+00	4506952	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminate: alpha-2,8-sialytransferase, GD3 synthase) (SIAT8) mRNA
4845	14726	24508	1.31	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4845	14726	24509	1.31	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4864	14734	24515	0.86	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4871	14751	24530	1.34	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4879	14759	24536	1.45	0.0E+00	AW452728.1	EST_HUMAN	UI-H-BI3-alv-f-02-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068691 3'
4885	14766	24542	1.2	0.0E+00	8922926	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
4886	14706	24490	7.99	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4888	14768	24544	2.81	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4888	14768	24546	2.81	0.0E+00	AF058332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4894	14774	24552	2.95	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4897	14777		4.34	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
4910	14789		2.58	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
4915	14794	24569	5.37	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4925	14804	24574	0.99	0.0E+00	AB028966.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4939	14817	24584	1.66	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4939	14817	24585	1.66	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4953	14830	24596	1.06	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4953	14830	24597	1.06	0.0E+00	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
4957	14013	23791	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4957	14013	23792	5.81	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4959	14834	24602	3.61	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4960	14835	24603	7.76	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4968	14843		1.17	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
4978	14853	24619	1.35	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
4987	14862		1.33	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
4990	14865		37.78	0.0E+00	D50657.1	NT	Homo sapiens gammma-cytoplasmic actin (ACTGP3) pseudogene
5000	14875	24639	2.29	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
5001	14876	24640	3.02	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5003	14878	24642	4.23	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	14013	23791	2.89	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5005	14013	23792	2.89	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5018	14892	24660	2.43	0.0E+00	X52988.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5037	14909	24681	1.84	0.0E+00	AF240635.1	NT	Homo.sapiens vascular endothelial cadherin 2 mRNA, complete cds
5037	14909	24682	1.84	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5040	14912	24686	1.01	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5054	14926	24698	1.22	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5055	14013	23791	11.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5055	14013	23792	11.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5056	14013	23791	14.9	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5056	14013	23792	14.9	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5065	14935	24708	1.33	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5070	14940	24713	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5070	14940	24714	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5071	14941	24715	1.06	0.0E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	14950	24726	3.04	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5096	14013	23791	6.27	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5096	14013	23792	6.27	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5098	14967	24743	1.34	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5098	14967	24744	1.34	0.0E+00	L35475.1	NT	Human olfactory receptor-like gene, complete cds
5099	14013	23791	9.38	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5099	14013	23792	9.38	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5124	14992	24765	0.94	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5126	14993	24766	1.35	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5130	14997	24768	0.8	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5140	15007	24778	1.06	0.0E+00	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5159	15026	24793	0.96	0.0E+00	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5162	15028	24794	1.59	0.0E+00	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5165	15031	24797	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5165	15031	24798	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5186	15050	24814	1.72	0.0E+00	AF006061.1	NT	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5187	14013	23791	10.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5187	14013	23792	10.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5189	15052	24816	6.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5193	15056		1.38	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5195	15058	24822	3.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5195	15058	24823	3.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5196	15059	24824	0.96	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
5208	15086		15.66	0.0E+00	AF093093.1	NT	Homo sapiens aconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5214	15137	24830	2.25	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5214	15137	24831	2.25	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5226	15150	24917	2.99	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDHA13), mRNA
5234	15158	24926	3.82	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5238	15162	24930	3.12	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5238	15162	24931	3.12	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5245	15168	24940	1.92	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5245	15168	24941	1.92	0.0E+00	X56163.1	NT	H.sapiens immunoglobulin heavy chain gene, variable region
5307	15228	25032	5.8	0.0E+00	BE675498.1	EST_HUMAN	7f10c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5308	15229	25033	1.77	0.0E+00	BE220753.1	EST_HUMAN	ht99a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194 3' similar to SW:Y054_HUMAN P42694 HYPOTHETICAL PROTEIN KIAA0054. ;
5309	15230	25034	1.67	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5309	15230	25035	1.67	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5311	15232	25037	5.46	0.0E+00	M29908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5313	15234	25038	1.81	0.0E+00	AI791363.1	EST_HUMAN	oh68a09.y5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1472152 5' similar to gb:M18512 IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
5319	19442	25044	5.42	0.0E+00	11421038	NT	Homo sapiens Sp4 transcription factor (SP4), mRNA
5324	15244		2.91	0.0E+00	BF665962.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5327	15247	25052	1.92	0.0E+00	BE538857.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5333	15253	25075	1.31	0.0E+00	BE292784.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5337	15257	25080	1.8	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5337	15257	25081	1.8	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5348	15987	26122	1.71	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5352	15272	25101	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5352	15272	25102	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5362	15282	25114	1.45	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5362	15282	25115	1.45	0.0E+00	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
5374	15294	25141	1.67	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5386	15305	25158	3.26	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
5386	15305	25159	3.26	0.0E+00	BF529931.1	EST_HUMAN	602042322F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179988 5'
5389	15308	25161	2.35	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5396	15315	25362	4.21	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5420	15341		2.43	0.0E+00	AW867316.1	EST_HUMAN	MR0-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5431	15351	25405	3.05	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5431	15351	25406	3.05	0.0E+00	BE292889.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5444	15365	25420	1.31	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5444	15365	25421	1.31	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5451	15372	25429	5.35	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5451	15372	25430	5.35	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5455	15376	25435	2.9	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5455	15376	25436	2.9	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5470	15390	25453	6.69	0.0E+00	M85719.1	EST_HUMAN	EST02238 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCM48
5474	15394	25459	3.67	0.0E+00	AW405472.1	EST_HUMAN	UI-HF-BL0-adh-d-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5489	15408	25471	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5489	15408	25472	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5489	15408	25473	5.74	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-h05 CT0263 Homo sapiens cDNA
5491	15410	25475	1.88	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5531	15448	25515	3.26	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
5532	15449	25516	1.5	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5532	15449	25517	1.5	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5537	15454	25524	2	0.0E+00	AI207616.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5548	15464	25534	3.98	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDHB2), mRNA
5555	15471	25542	6.76	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5556	15472	25543	1.58	0.0E+00	10048478	NT	Mus musculus aczonin (Acz), mRNA
5557	15473	25544	3.03	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5557	15473	25545	3.03	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5564	15480	25553	2.1	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321 5'
5566	15482	25555	2.93	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5574	15489	25566	1.74	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
5596	15510	25588	2.47	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
5597	15511	25589	1.89	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
5601	15516	25593	1.41	0.0E+00	BE958636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
5615	15530	25613	1.66	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
5615	15530	25614	1.66	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
5631	15545	25633	1.54	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5631	15545	25634	1.54	0.0E+00	W33069.1	EST_HUMAN	zc08h06.r1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
5632	15546		2.16	0.0E+00	AF012618.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
5634	15548	25636	3.57	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
5638	15551	25642	2.74	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
5649	15561	25654	1.63	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5649	15561	25655	1.63	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5660	19450	25668	10.66	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
5663	15574	25671	1.29	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
5663	15574	25672	1.29	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
5680	15589	25690	13.03	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5680	15589	25691	13.03	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
5730	15638	25742	1.41	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
5741	15649	25756	3.4	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
5755	15663	25770	4.14	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
5756	15664	25771	3.57	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5756	15664	25772	3.57	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
5775	15682	25790	2.8	0.0E+00	BE257173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
5784	15690	25800	1.47	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
5795	15701	25811	1.38	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
5826	15732		8.1	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
5830	15736	25848	2.81	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BL0-aco-g-12-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'
5832	15738	25850	4.21	0.0E+00	H01255.1	EST_HUMAN	yj27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
5838	15744	25857	1.99	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
5843	15749	25862	4.25	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5843	15749	25863	4.25	0.0E+00	BE735989.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
5847	15753	25869	11.57	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5847	15753	25870	11.57	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
5854	15760	25878	1.56	0.0E+00	AI989483.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'
5859	15765	25882	4.81	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
5859	15765	25883	4.81	0.0E+00	BE293153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963 5'
5901	15807	25931	1.36	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
5901	15807	25932	1.36	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-aco-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
5921	15826	25951	1.69	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLCEHC06 5'
5930	15835	25958	2.24	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
5936	15841	25964	3.45	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
5936	15841	25965	3.45	0.0E+00	AW163640.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206 ;
5951	15856	25978	4.79	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
5955	15860	25981	7.23	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5955	15860	25982	7.23	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
5961	15866	25988	3.71	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
5964	15869	25991	2.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5964	15869	25992	2.15	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5970	15875	25999	3.54	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
5973	15877	26001	4.13	0.0E+00	AI638412.1	EST_HUMAN	tt31f11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR. ;
5974	15878	26002	1.79	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
5980	15885	26007	3.58	0.0E+00	AA434584.1	EST_HUMAN	zw52c03.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773668 5'
5991	15896	26019	1.48	0.0E+00	BE925875.1	EST_HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA
6011	15916	26044	1.44	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6041	15944	26076	7.44	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6042	15945	26077	1.81	0.0E+00	BF085667.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6063	16046	26191	3.15	0.0E+00	AA190755.1	EST_HUMAN	zp88e03.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6071	16054	26201	6.08	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6071	16054	26202	6.08	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6076	16059	26208	3.07	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
6094	15104	24867	1.98	0.0E+00	BE566381.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
6099	15109	24872	13.15	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6099	15109	24873	13.15	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6101	15995	26130	2.07	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
6101	15995	26131	2.07	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95. ;
6118	16012	26150	1.46	0.0E+00	BF088376.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
6121	16015	26153	3.84	0.0E+00	AA195106.1	EST_HUMAN	zr34g03.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'
6126	15973		10.28	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
6135	15982	26118	2.57	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6142	15990		2.32	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
6146	16019	26157	2.8	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6146	16019	26158	2.8	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6154	15112	24876	2.75	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
6168	15125	24842	5.63	0.0E+00	BE262941.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
6169	15126	24843	2.32	0.0E+00	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6169	15126	24844	2.32	0.0E+00	Z37976.1	NT	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6170	15127	24845	2.83	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6170	15127	24846	2.83	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6175	15132	24851	1.35	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6178	16064	26213	2.18	0.0E+00	BF569905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6181	16067	26217	3.58	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
6190	16075	26224	5.61	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
6193	16078	26227	1.76	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6225	16091	26241	1.34	0.0E+00	AW954806.1	EST_HUMAN	EST366876 MAGE resequences, MAGC Homo sapiens cDNA
6226	16092	26242	1.41	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6237	16103	26253	5.9	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
6253	16119		2.44	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
6260	16126	26279	1.31	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
6260	16126	26280	1.31	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
6273	15137	24830	1.97	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6273	15137	24831	1.97	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6286	16150	26305	3.63	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
6286	16150	26306	3.63	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25- dihydroxyvitamin D3) receptor (VDR), mRNA
6302	16166	26323	25.51	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element ;
6302	16166	26324	25.51	0.0E+00	AI128344.1	EST_HUMAN	qc67a07.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element ;
6304	16168	26326	18.73	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6304	16168	26327	18.73	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6306	16170		14.06	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5'
6308	16172	26329	5.1	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 G806562 NEBULIN. ;
6328	16191	26353	6.72	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6328	16191	26354	6.72	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6337	16200	26360	7.55	0.0E+00	X70172.1	NT	H.sapiens DNA for ZNGP2 pseudogene, exon 4
6339	16202	26362	11:09	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6339	16202	26363	11.09	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6347	16210	26372	1.43	0.0E+00	AW956503.1	EST_HUMAN	EST368573 MAGE resequences, MAGD Homo sapiens cDNA
6349	16212	26374	2.54	0.0E+00	AW950516.1	EST_HUMAN	EST362586 MAGE resequences, MAGA Homo sapiens cDNA
6389	16251	26411	1.67	0.0E+00	AW239326.1	EST_HUMAN	xb39a05.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050 HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
6400	16261		1.8	0.0E+00	AU117553.1	EST_HUMAN	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
6401	16262	26422	3.64	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
6411	16272	26434	54.65	0.0E+00	AA211663.1	EST_HUMAN	zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
6462	16321	26486	4.25	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6462	16321	26487	4.25	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
6499	16358	26530	1.59	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
6499	16358	26531	1.59	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
6516	16374	26551	1.3	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6530	16389	26569	1.98	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6534	16392	26571	5.37	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
6539	16397	26576	2.98	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
6550	16408	26586	6.49	0.0E+00	4501848	NT	*Homo sapiens* ATP-*binding cassette, sub-family* A (ABC1), *member 3* (ABCA3), mRNA
6555	16413	26590	4.97	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
6555	16413	26591	4.97	0.0E+00	BE739870.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
6556	16414	26592	60.88	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
6556	16414	26593	60.88	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
6574	16432	26614	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6574	16432	26615	1.52	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
6622	16502	26690	1.29	0.0E+00	AA149791.1	EST_HUMAN	zo01c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
6645	16525	26719	3.72	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
6654	16534	26729	3.97	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6654	16534	26730	3.97	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6674	16554	26749	1.65	0.0E+00	AA397551.1	EST_HUMAN	zt81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG {RETROVIRAL ELEMENT} ;
6677	16557	26750	7.54	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
6688	16568		8.73	0.0E+00	BF673096.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
6714	16594	26783	1.96	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
6714	16594	26784	1.96	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
6730	16610		1.31	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
6742	16621	26810	1.35	0.0E+00	AW500549.1	EST_HUMAN	UI-HF-BN0-akj-f-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077496 5'
6747	16626	26813	14.35	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1] ;
6776	16654	26842	1.16	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
6775	16654	26843	1.16	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
6783	16662	26852	2.72	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudoautosomal region; segment 1/2
6810	16689	26878	2.2	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95793 O95793 STAUFEN PROTEIN. ;
6811	16690	26879	1.36	0.0E+00	AI885671.1	EST_HUMAN	wl60b10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
6817	16696	26887	1.31	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
6817	16696	26888	1.31	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
6824	16703	26897	1.44	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6824	16703	26898	1.44	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
6851	16730		3.89	0.0E+00	AA398511.1	EST_HUMAN	zt73a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
6856	16735	26928	1.45	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
6856	16735	26929	1.45	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
6869	16748	26942	1.21	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
6869	16748	26943	1.21	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
6879	16758	26956	1.25	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6879	16758	26957	1.25	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6899	16778		2.01	0.0E+00	BE890797.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
6913	16791	26984	2.4	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
6913	16791	26985	2.4	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
6955	16833	27026	2.85	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
6955	16833	27027	2.85	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
6955	16833	27028	2.85	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
6993	16870		1.36	0.0E+00	AW513513.1	EST_HUMAN	xo46e01.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
6995	16872	27063	3.64	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
7011	16888	27081	4.46	0.0E+00	BE378495.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
7015	16892	27083	1.31	0.0E+00	AA410545.1	EST_HUMAN	zt32e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'
7016	16893		4.32	0.0E+00	BF313946.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
7021	16898	27088	1.41	0.0E+00	AW139673.1	EST_HUMAN	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
7021	16898	27089	1.41	0.0E+00	AW139673.1	EST_HUMAN	UI-H-BI1-adr-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
7038	16915	27104	2.39	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
7040	16917	27106	1.83	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7040	16917	27107	1.83	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
7040	16917	27108	1.83	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
7069	16946	27137	6.35	0.0E+00	AA962527.1	EST_HUMAN	or80g02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
7073	16950	27142	3.54	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
7073	16950	27143	3.54	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
7088	16965	27159	1.28	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
7095	16972		1.45	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAAF11 5'
7099	16976	27169	3.64	0.0E+00	AW337277.1	EST_HUMAN	xw73c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587 INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
7102	16979	27171	1.57	0.0E+00	AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
7147	17024	27218	2.64	0.0E+00	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7148	17025	27219	4.41	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
7148	17025	27220	4.41	0.0E+00	AW592233.1	EST_HUMAN	hf48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096 3'
7176	17053	27241	2.84	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
7176	17053	27242	2.84	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
7177	17054	27243	1.17	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
7178	17055	27244	18.6	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
7198	17075	27261	3.97	0.0E+00	11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA
7204	17081	27268	1.25	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
7207	17084	27272	2.65	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
7207	17084	27273	2.65	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
7210	17087	27277	1.96	0.0E+00	AV660739.1	EST_HUMAN	AV660739 GLC Homo sapiens cDNA clone GLCGKG12 3'
7213	17090	27280	3.43	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
7231	17108	27298	3.86	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
7231	17108	27299	3.86	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
7241	17118	27313	1.91	0.0E+00	X14766.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
7250	17127	27320	2.12	0.0E+00	AI954607.1	EST_HUMAN	wq34a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MGB3_HUMAN O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
7254	17131	27324	4.49	0.0E+00	9256595	NT	Homo sapiens protocadherin alpha 8 (PCDHA8), mRNA
7263	17140	27333	1.54	0.0E+00	AW958311.1	EST_HUMAN	EST370381 MAGE resequences, MAGE Homo sapiens cDNA
7269	17146	27340	1.49	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
7280	17157	27352	6.88	0.0E+00	11436995	NT	Homo sapiens MAP-kinase activating death domain (MADD), mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7290	17166	27365	1.44	0.0E+00	AB011150.1	NT	Homo sapiens mRNA *for* KIAA0578 protein, partial cds
7291	17167	27366	2.56	0.0E+00	BE794823.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
7298	17174	27374	1.24	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
7298	17174	27376	1.24	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
7308	17184	27383	1.6	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
7308	17184	27384	1.6	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
7360	17227	27426	1.38	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
7360	17227	27427	1.38	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL *mRNA, complete cds* (MOUSE);
7368	17346	27551	2.71	0.0E+00	BF348013.1	EST_HUMAN	602023150F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158300 5'
7383	17252	27457	3	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
7406	17273	27479	11.81	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
7425	17292	27503	1.27	0.0E+00	AI088043.1	EST_HUMAN	ow60h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN. ;
7429	16442	26628	2.06	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7429	16442	26629	2.06	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7431	16444	26632	8.86	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;
7431	16444	26633	8.86	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN P29316 60S RIBOSOMAL PROTEIN L23A. ;
7432	16445	26634	1.69	0.0E+00	AW953836.1	EST_HUMAN	EST366026 MAGE resequences, MAGC Homo sapiens cDNA
7450	17259	27464	3.92	0.0E+00	AF153466.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
7461	17321		4.9	0.0E+00	BE255829.1	EST_HUMAN	601109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
7463	17323	27529	1.37	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
7463	17323	27530	1.37	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
7464	17324	27531	7.21	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
7475	17335	27541	2.85	0.0E+00	BE263191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
7488	17358	27562	3.98	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
7488	17358	27563	3.98	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
7490	17360	27566	3.22	0.0E+00	BE746215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
7499	17369	27574	1.93	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 *(organic anion transporter), member 9 (SLC21A9), mRNA*
7499	17369	27575	1.93	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7499	17369	27576	1.93	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
7514	17302	27509	1.47	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
7530	17381	27591	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7530	17381	27592	2.59	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7548	17399	27612	1.47	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
7559	17410	27626	1.76	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
7559	17410	27627	1.76	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
7563	17414	27629	1.25	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7563	17414	27630	1.25	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7580	17431	27645	2.46	0.0E+00	AW500526.1	EST_HUMAN	UI-HF-BN0-akj-c-07-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
7607	17458	27673	1.34	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
7621	17472	27691	2.56	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7621	17472	27692	2.56	0.0E+00	S78466.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
7622	17473	27693	2.57	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
7630	17481	27701	1.62	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
7650	17500	27722	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7650	17500	27723	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7659	17509	27734	7.73	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7659	17509	27735	7.73	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7666	17516	27743	1.76	0.0E+00	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7682	17532	27756	2.22	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
7683	17533	27757	1.86	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
7701	17551	27776	2.72	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
7701	17551	27777	2.72	0.0E+00	AF009220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
7708	17558	27784	1.65	0.0E+00	BF092898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
7720	17570	27795	2.44	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
7728	17578	27800	1.74	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
7736	17586	27810	1.91	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
7753	17603	27826	5.98	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
7753	17603	27827	5.98	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 *Homo sapiens* cDNA clone Y79AA1002307 5'
7756	17606	27830	7.52	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
7758	17608	27832	2.48	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7758	17608	27833	2.48	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7785	17635	27868	2.96	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7785	17635	27869	2.96	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7795	17645	27879	2.13	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
7795	17645	27880	2.13	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
7804	17654	27892	4.01	0.0E+00	AA196387.1	EST_HUMAN	zp97h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
7823	17673	27915	1.17	0.0E+00	AA131248.1	EST_HUMAN	zl31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
7823	17673	27916	1.17	0.0E+00	AA131248.1	EST_HUMAN	zl31f01.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
7842	17692	27937	1.46	0.0E+00	AF179308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, *complete cds*
7865	17715	27959	3.45	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7865	17715	27960	3.45	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7892	17742	27985	1.24	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
7897	17747	27987	1.64	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
7903	17753	27991	5.19	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
7903	17753	27992	5.19	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
7904	17754	27993	3.27	0.0E+00	AA194770.1	EST_HUMAN	zq06h11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628965 5' similar to TR:G407097 G407097 165KD PROTEIN. ;
7905	17755	27994	5.43	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
7905	17755	27995	5.43	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184939 5'
7946	17796	28036	1.37	0.0E+00	T03078.1	EST_HUMAN	FB23A4 *Fetal brain*, Stratagene Homo sapiens cDNA clone *FB23A4* 3'end
7972	17822	28065	2.35	0.0E+00	BF436218.1	EST_HUMAN	nab45e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
7973	17823		2.05	0.0E+00	AV654765.1	EST_HUMAN	AV654765 GLC Homo sapiens cDNA clone GLCDZC07 3'
7982	17832	28072	3.55	0.0E+00	AW517960.1	EST_HUMAN	xu74b01.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:M69066 MOESIN (HUMAN);
7984	17834	28074	6.06	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
8001	17851	28092	1.65	0.0E+00	BE781742.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
8008	17858	28101	2.23	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
8008	17858	28102	2.23	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-d03 BT0642 Homo sapiens cDNA
8015	17865	28111	1.69	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
8015	17865	28112	1.69	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
8032	17924	28170	2.33	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8032	17924	28171	2.33	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
8034	17926		6.11	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
8040	17931	28178	6.43	0.0E+00	AW963563.1	EST_HUMAN	EST375636 MAGE resequences, MAGH Homo sapiens cDNA
8051	17942	28191	2.5	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8051	17942	28192	2.5	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8054	17945	28195	1.99	0.0E+00	AW057621.1	EST_HUMAN	wy61f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60566 VDX ;
8059	17950	28200	1.92	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0917
8060	17951	28201	4.86	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ;
8060	17951	28202	4.86	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element ;
8068	17959	28209	2.91	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
8068	17959	28210	2.91	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
8081	17972	28221	2.01	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BL0-acm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
8084	17975	28224	4.8	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
8085	17976	28225	9.16	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
8085	17976	28226	9.16	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
8086	17977	28227	2.73	0.0E+00	AI991827.1	EST_HUMAN	wu32b06.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
8089	17980	28231	3.04	0.0E+00	BE882109.1	EST_HUMAN	601505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
8093	17984	28233	10.56	0.0E+00	BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
8095	17986	28234	22.36	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
8095	17986	28235	22.36	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
8110	18000	28247	1.91	0.0E+00	BE903304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
8113	15448	25516	4.05	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8134	18022	28269	4.69	0.0E+00	BE793498.1	EST_HUMAN	601588829F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
8143	18031	28277	6.8	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
8143	18031	28278	6.8	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
8156	18044	28296	17.96	0.0E+00	AW516055.1	EST_HUMAN	xy04g10.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
8161	18049	28301	2.17	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLACE1002794 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	.Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8166	18054	28304	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8166	18054	28305	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8166	18054	28306	3.45	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element ;
8168	18056	28307	1.82	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
8169	18057	28308	2.8	0.0E+00	F13069.1	EST_HUMAN	HSC3IC031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
8176	18064	28313	2.12	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
8191	18077	28328	2.92	0.0E+00	AW338094.1	EST_HUMAN	xw66f01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17115 IG MU CHAIN C REGION (HUMAN);
8192	18078	28329	5.64	0.0E+00	AW451230.1	EST_HUMAN	UI-H-BI3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
8192	18078	28330	5.64	0.0E+00	AW451230.1	EST_HUMAN	UI-H-BI3-alh-a-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
8194	10179		14.21	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
8196	18081	28332	2.03	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
8208	18092	28346	2.35	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
8224	18106	28359	1.88	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
8227	18109	28363	59.52	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
8240	18120	28371	3.47	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
8241	18121		25.37	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
8244	18124	28374	6.16	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
8245	18125		2.72	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
8250	18130	28378	6.77	0.0E+00	AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
8250	18130	28379	6.77	0.0E+00	AI149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
8251	18131	28380	3.05	0.0E+00	AW391937.1	EST_HUMAN	QV4-ST0234-121199-032-b06 ST0234 Homo sapiens cDNA
8262	18142		4.62	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
8265	18145	28386	18.63	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR), mRNA
8271	18151	28392	1.78	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
8271	18151	28393	1.78	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-d06 UM0093 Homo sapiens cDNA
8272	18152	28394	2.14	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184979 5'
8273	18153	28395	49.5	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
8282	18161	28403	2.53	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
8283	18162	28404	68.7	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8287	18166	28409	3.52	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8287	18166	28410	3.52	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-f07 FT0134 Homo sapiens cDNA
8307	18184	28431	24.55	0.0E+00	AA740782.1	EST_HUMAN	ob32e07.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element ;
8313	18190	28439	3.12	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
8326	18203	28452	149.55	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC4817
8333	18210	28460	2.17	0.0E+00	AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
8333	18210	28461	2.17	0.0E+00	AA746375.1	EST_HUMAN	oa56h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
8341	18218	28470	2.41	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
8341	18218	28471	2.41	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
8344	18221	28472	1.82	0.0E+00	BF353625.1	EST_HUMAN	QV2-HT0698-020800-295-d07 HT0698 Homo sapiens cDNA
8345	18222	28473	8.08	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
8357	18234	28482	10.53	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
8375	18252	28503	1.86	0.0E+00	BF366553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
8395	18271	28523	3.78	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8395	18271	28524	3.78	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0645-060500-002-E05 HT0645 Homo sapiens cDNA
8405	18281	28533	3.46	0.0E+00	BE896423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
8410	18285	28539	1.74	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
8410	18285	28540	1.74	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
8442	18316	28574	4	0.0E+00	BE897953.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
8443	18317	28575	1.96	0.0E+00	AI459545.1	EST_HUMAN	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
8443	18317	28576	1.96	0.0E+00	AI459545.1	EST_HUMAN	ao86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
8455	18328	28587	88.73	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
8455	18328	28588	88.73	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
8480	18353	28618	3.88	0.0E+00	4758827	NT	Homo sapiens neurexin III (NRXN3) mRNA
8481	18354	28619	4.54	0.0E+00	BF206561.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
8483	18356	28620	16	0.0E+00	AW207734.1	EST_HUMAN	UI-H-BI2-age-h-01-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
8484	18357	28621	3.77	0.0E+00	AW604975.1	EST_HUMAN	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
8484	18357	28622	3.77	0.0E+00	AW604975.1	EST_HUMAN	RC0-CT0380-210100-032-c10 CT0380 Homo sapiens cDNA
8488	18361	28625	6.91	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
8488	18361	28626	6.91	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8490	18363	28628	2.59	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
8490	18363	28629	2.59	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
8511	18383	28648	2.85	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
8514	18386	28651	2.01	0.0E+00	BF093687.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
8518	18390	28653	2.9	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
8518	18390	28654	2.9	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
8526	18398	28665	6.47	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8546	18418	28687	4.47	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
8546	18418	28688	4.47	0.0E+00	BF507876.1	EST_HUMAN	UI-H-BI4-aok-b-10-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
8553	18423	28692	2.16	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone PLACE1001381 5'
8557	18427	28696	5.62	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
8557	18427	28697	5.62	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
8566	18435		10.32	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
8577	18445	28713	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
8577	18445	28714	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
8581	18449	28717	3.49	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
8581	18449	28718	3.49	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
8596	18463	28734	6.1	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
8603	18470	28741	2.49	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
8605	18472	28744	5.44	0.0E+00	AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
8608	18475		120.65	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
8612	18479	28750	3.18	0.0E+00	AI660968.1	EST_HUMAN	wf20e11.x1 Soares_Dieckgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8614	18481	28752	3.64	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8614	18481	28753	3.64	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
8620	18486	28758	26.88	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
8639	18504		4.07	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
8648	18512	28793	2.89	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
8650	18514		2.24	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
8661	18550	28833	4.61	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8661	18550	28834	4.61	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN. ;
8663	18552	28836	3	0.0E+00	AW753028.1	EST_HUMAN	QV0-CT0225-101299-071-f06 CT0225 Homo sapiens cDNA
8668	18557		2.36	0.0E+00	AA558707.1	EST_HUMAN	nl42c08.s1 NCI_CGAP_Pr4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
8669	15148	24916	5	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
8670	18558	28842	7.41	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
8700	18518	28800	4.73	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-f05 HT0731 Homo sapiens cDNA
8712	18529	28812	4.74	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
8712	18529	28813	4.74	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G178 5'
8722	18539	28823	12.53	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
8724	18580	28863	4.18	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
8724	18580	28864	4.18	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686 Q13686 ALKB HOMOLOG PROTEIN. ;
8728	18584	28869	2.33	0.0E+00	BE910546.1	EST_HUMAN	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'
8737	17886	28130	5.67	0.0E+00	BE676347.1	EST_HUMAN	7f27f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1. ;
8772	18589	28875	2.78	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8772	18589	28876	2.78	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
8784	18599	28888	4.02	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
8797	18611	28902	1.91	0.0E+00	BE622317.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
8827	18640	28924	10.47	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8827	18640	28925	10.47	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
8837	18650	28937	2.97	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8837	18650	28938	2.97	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8840	18653	28941	2.35	0.0E+00	AW006022.1	EST_HUMAN	wz91h01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2 CE11040 ZINC FINGER, C2H2 TYPE ;
8843	19474	28943	3.84	0.0E+00	BF002333.1	EST_HUMAN	7h22b10.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO. ;
8861	18673	28962	3.19	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
8861	18673	28963	3.19	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
8878	18690	28982	2.57	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8878	18690	28983	2.57	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8883	18694	28987	5.52	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
8885	18696	28989	2.04	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8885	18696	28990	2.04	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
8896	16272	26434	63.21	0.0E+00	AA211663.1	EST_HUMAN	zn56f02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8900	15883	26006	4.08	0.0E+00	AW505430.1	EST_HUMAN	UI-HF-BN0-ama-c-01-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
8902	18710	29005	3.25	0.0E+00	BE794758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8903	18711	29006	37.53	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
8904	18712	29007	2.93	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8915	18723	29014	6.35	0.0E+00	BE409993.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629544 5'
8916	18724	29015	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	29016	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	29017	1.93	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8917	18725	29018	2.32	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8917	18725	29019	2.32	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8919	18727	29020	5.66	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
8919	18727	29021	5.66	0.0E+00	BF681641.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4296725 5'
8924	18732	29026	3.22	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
8933	18741	29034	6.15	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
8933	18741	29035	6.15	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
8934	18742	29036	3.02	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8934	18742	29037	3.02	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8964	19475		20.36	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
8965	18771	29062	1.98	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
8965	18771	29063	1.98	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
8969	18775	29066	31.56	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532968 5'
8981	18786	29076	36.47	0.0E+00	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8981	18786	29077	36.47	0.0E+00	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8982	18787	29078	34.29	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
8987	18792	29081	31.52	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
8987	18792	29082	31.52	0.0E+00	F00884.1	EST_HUMAN	HSB77E122 STRATAGENE Human skeletal muscle cDNA library, cat. #936215. Homo sapiens cDNA clone 77E12
9000	18803	29096	7.35	0.0E+00	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
9002	18805	29098	92.9	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
9017	19747	24893	2.54	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
9031	19594		2.67	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9033	19605		3.43	0.0E+00	AI190993.1	EST_HUMAN	qe17b12.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
9043	18829		2.24	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
9062	18843		2.2	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9071	18849		2.73	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9090	18864		5.48	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
9123	19563	25066	1.63	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9133	19571		2.82	0.0E+00	AL041931.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434K0819 5'
9158	19711		3.07	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
9167	18910		4.39	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G218 5'
9180	19610		2.36	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
9218	19732		1.3	0.0E+00	N54484.1	EST_HUMAN	yv40e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
9233	18952		3.36	0.0E+00	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
9236	10752	20601	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
9236	10752	20602	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
9246	19612		2.75	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
9276	10477		2.7	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidroitic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9309	19412	25183	2.48	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9370	19544	25064	3.23	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element;contains element MER22 repetitive element ;
9382	19595		1.61	0.0E+00	BE090210.1	EST_HUMAN	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA
9426	19607		2.33	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
9461	19092		1.56	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9498	19600		1.59	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
9529	19136		1.58	0.0E+00	AI904646.1	EST_HUMAN	QV-BT065-020399-103 BT065 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9540	19596		1.68	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
9551	11841	21724	1.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9551	11841	21725	1.98	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9571	19161	25267	2.33	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
9584	11561	21426	2.87	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
9584	11561	21427	2.87	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYLTRANSPEPTIDASE 5 PRECURSOR (HUMAN);
9597	19179		32.21	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
9599	19181	25244	3.99	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9599	19181	25245	3.99	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9685	19239	25214	5.21	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
9692	15089	24829	1.64	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
9698	19249		2.39	0.0E+00	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9721	15092	24886	3.19	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
9734	19269		2.21	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9773	19291	25233	1.5	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
9794	19757		2.79	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9800	10546	20354	1.41	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9878	19364		2.13	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
9913	·19388	25177	2.42	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
9938	19407		1.51	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
9946	19621		1.29	0.0E+00	11434874	NT	Homo sapiens oxytocin receptor (OXTR), mRNA
9966	19591		1.56	0.0E+00	BE177449.1	EST_HUMAN	RC1-HT0595-200400-012-f12 HT0595 Homo sapiens cDNA
9971	19431		1.28	0.0E+00	AL048911.1	EST_HUMAN	DKFZp434J0618_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0618

CLAIMS

1. A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.

3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.

4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.

5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.

6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.

7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and then

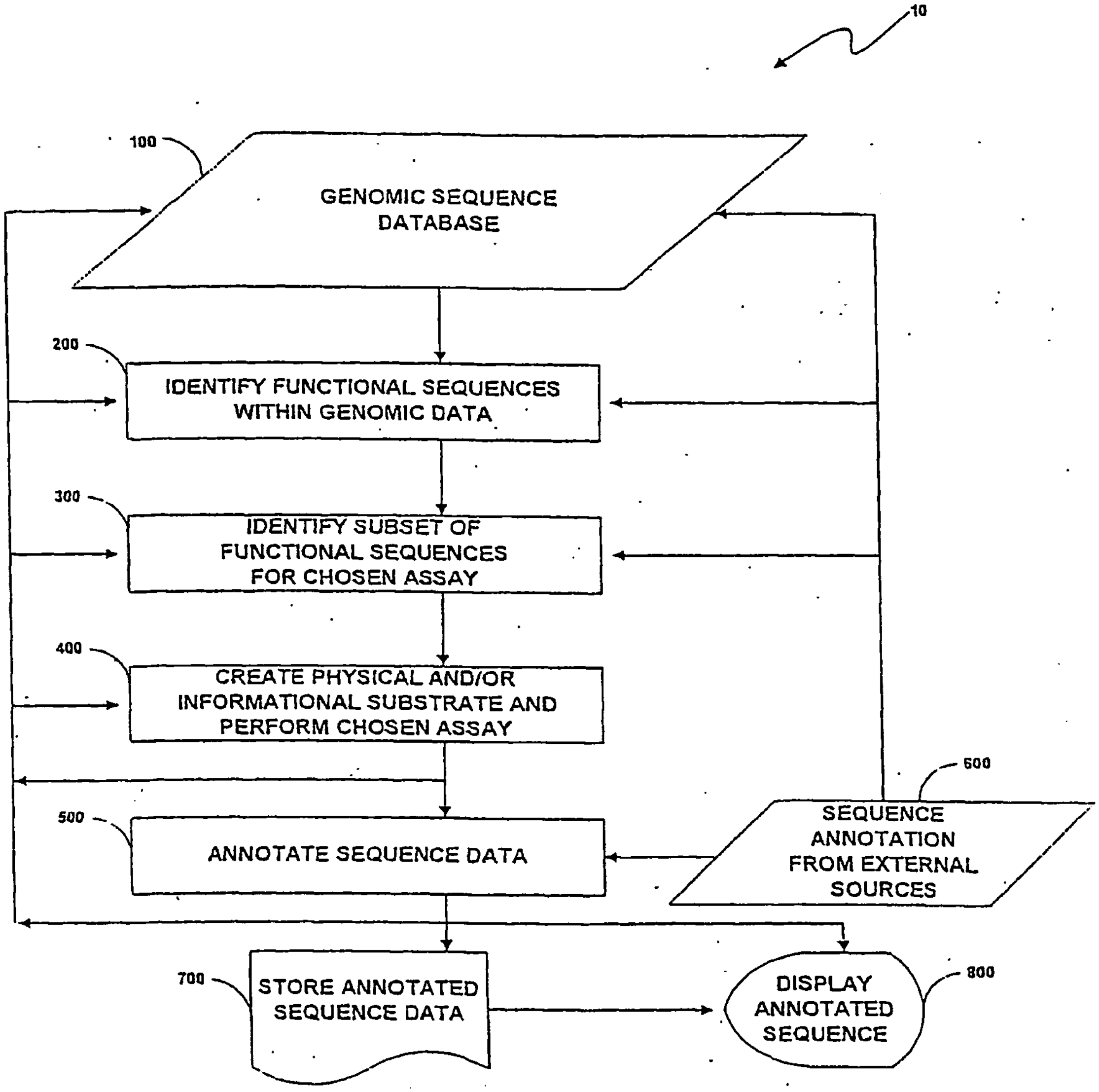
measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 19,771 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 19,771.

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 19,772 - 29,119.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GENOMIC SEQUENCE DATABASE
200
IDENTIFY FUNCTIONAL SEQUENCES WITHIN GENOMIC DATA
300
IDENTIFY SUBSET OF FUNCTIONAL SEQUENCES FOR CHOSEN ASSAY
400
CREATE PHYSICAL AND/OR INFORMATIONAL SUBSTRATE AND PERFORM CHOSEN ASSAY
500
ANNOTATE SEQUENCE DATA
600
SEQUENCE ANNOTATION FROM EXTERNAL SOURCES
700
STORE ANNOTATED SEQUENCE DATA
800
DISPLAY ANNOTATED SEQUENCE

Fig. 1

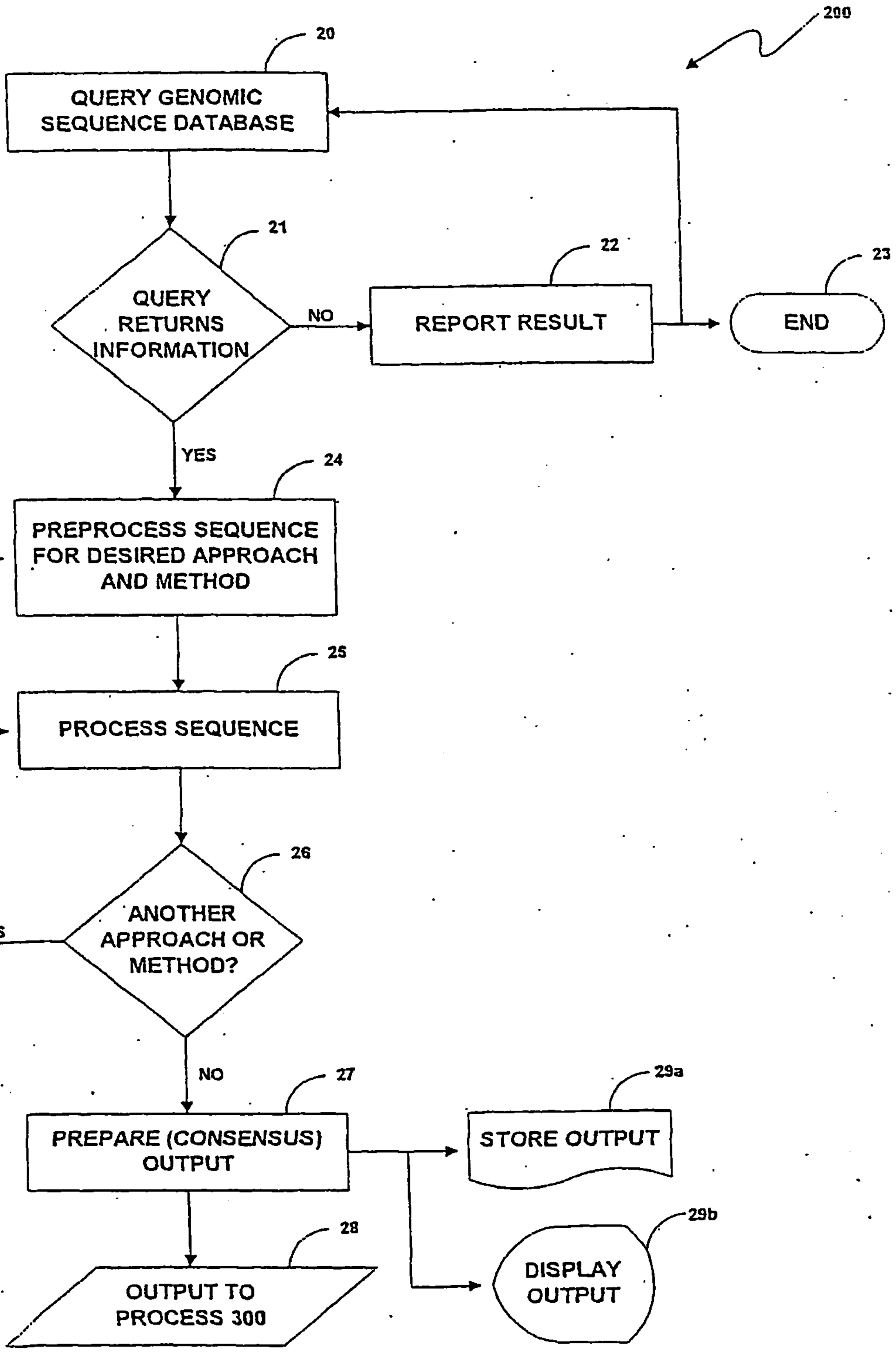
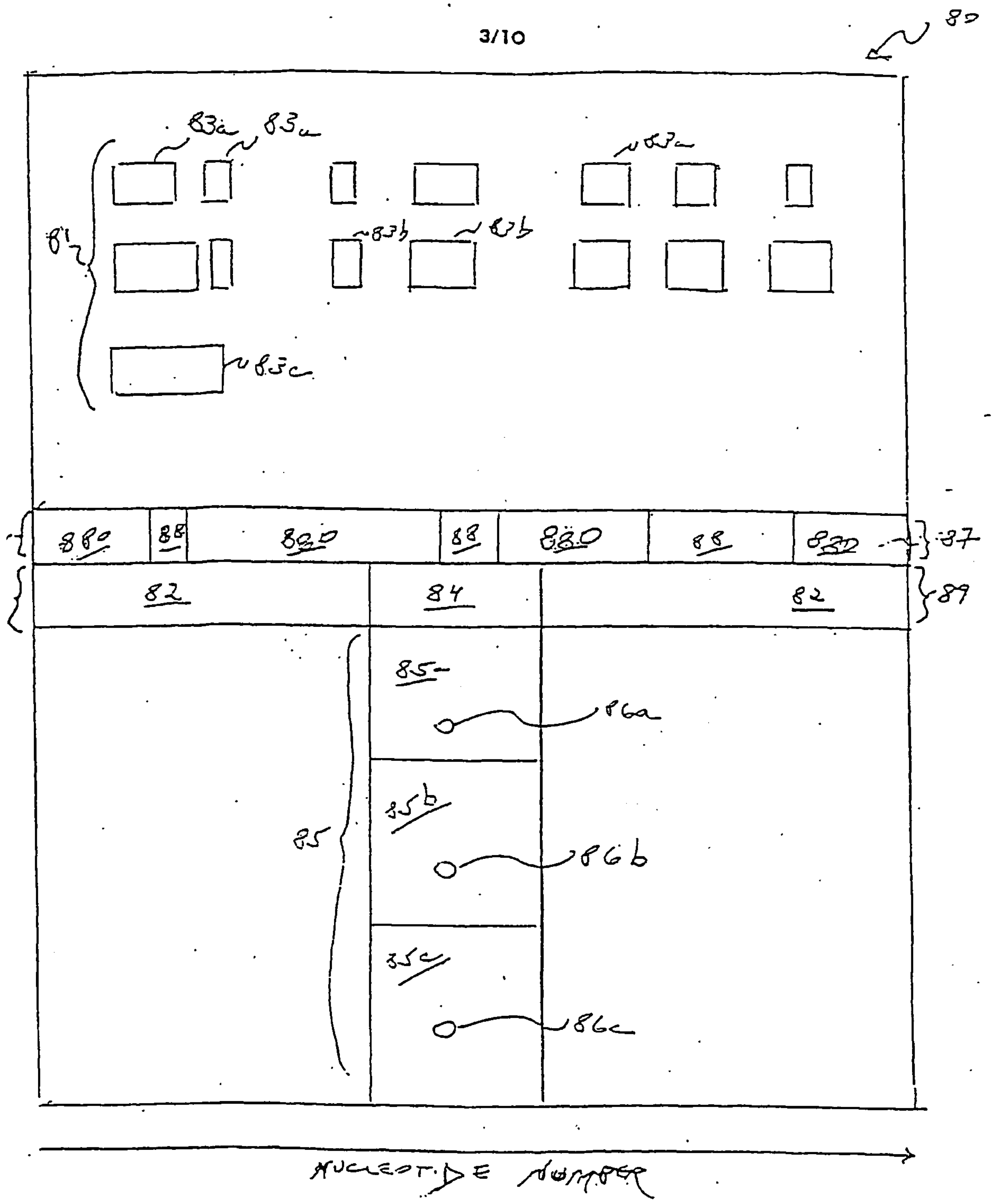

200
20
QUERY GENOMIC SEQUENCE DATABASE
21
QUERY RETURNS INFORMATION
NO
22
REPORT RESULT
23
END
YES
24
PREPROCESS SEQUENCE FOR DESIRED APPROACH AND METHOD
25
PROCESS SEQUENCE
26
ANOTHER APPROACH OR METHOD?
YES
NO
27
PREPARE (CONSENSUS) OUTPUT
29a
STORE OUTPUT
29b
DISPLAY OUTPUT
28
OUTPUT TO PROCESS 300

Fig. 2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83a
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81
83b
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88
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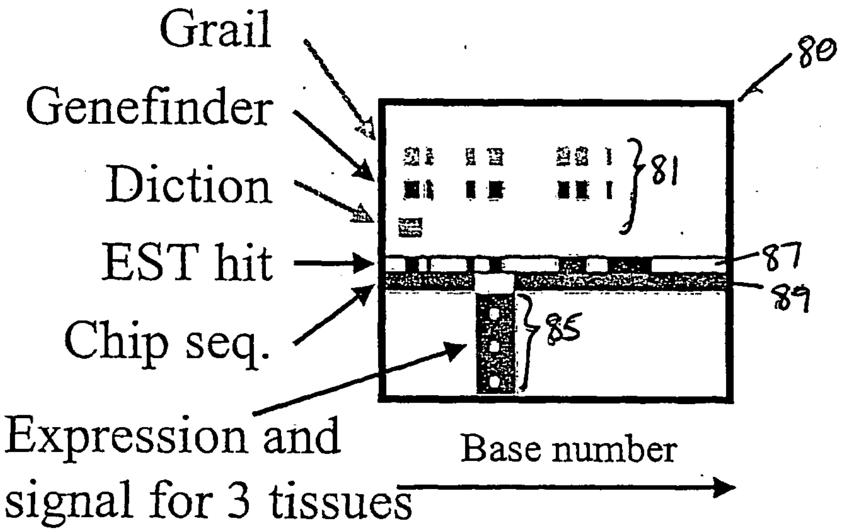
84
82
89
85a
86a
85
85b
86b
85c
86c
NUCLEOTIDE NUMBER

Fig. 3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Genefinder
Diction
EST hit
Chip seq.
Expression and signal for 3 tissues
Base number
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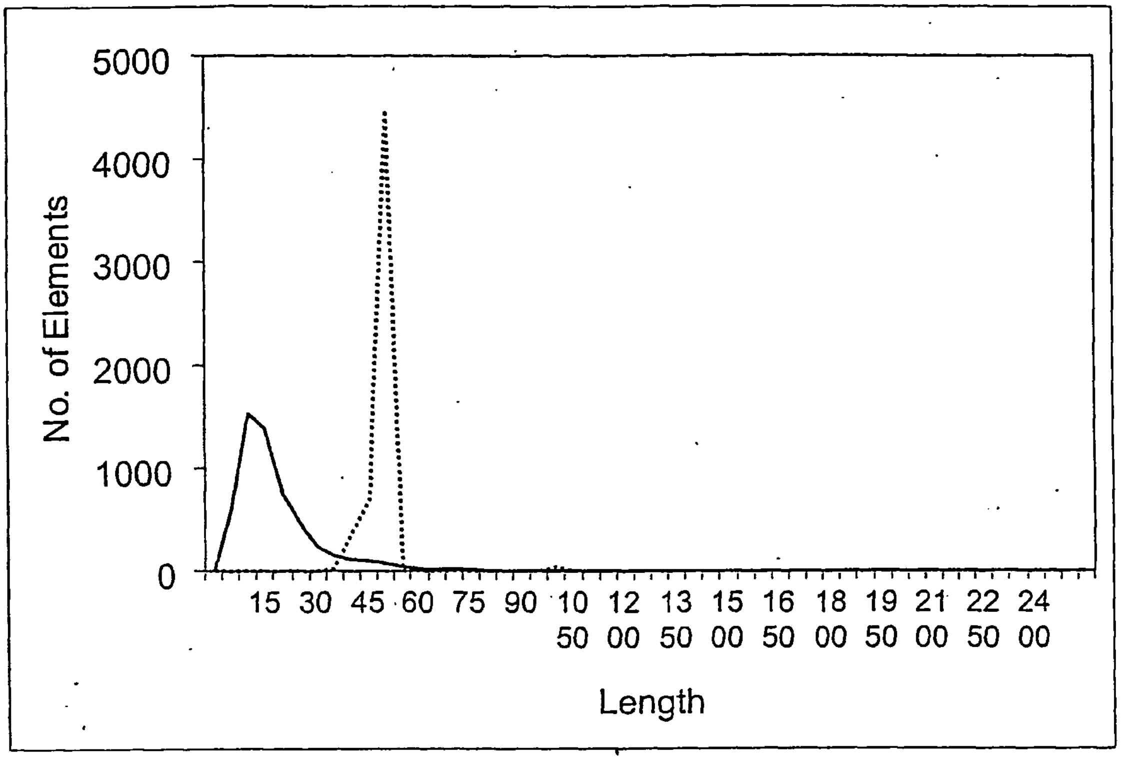
81
87
89
85

Fig. 4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4000
3000
2000
1000
0
No. of Elements
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30
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10 50
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13 50
15 00
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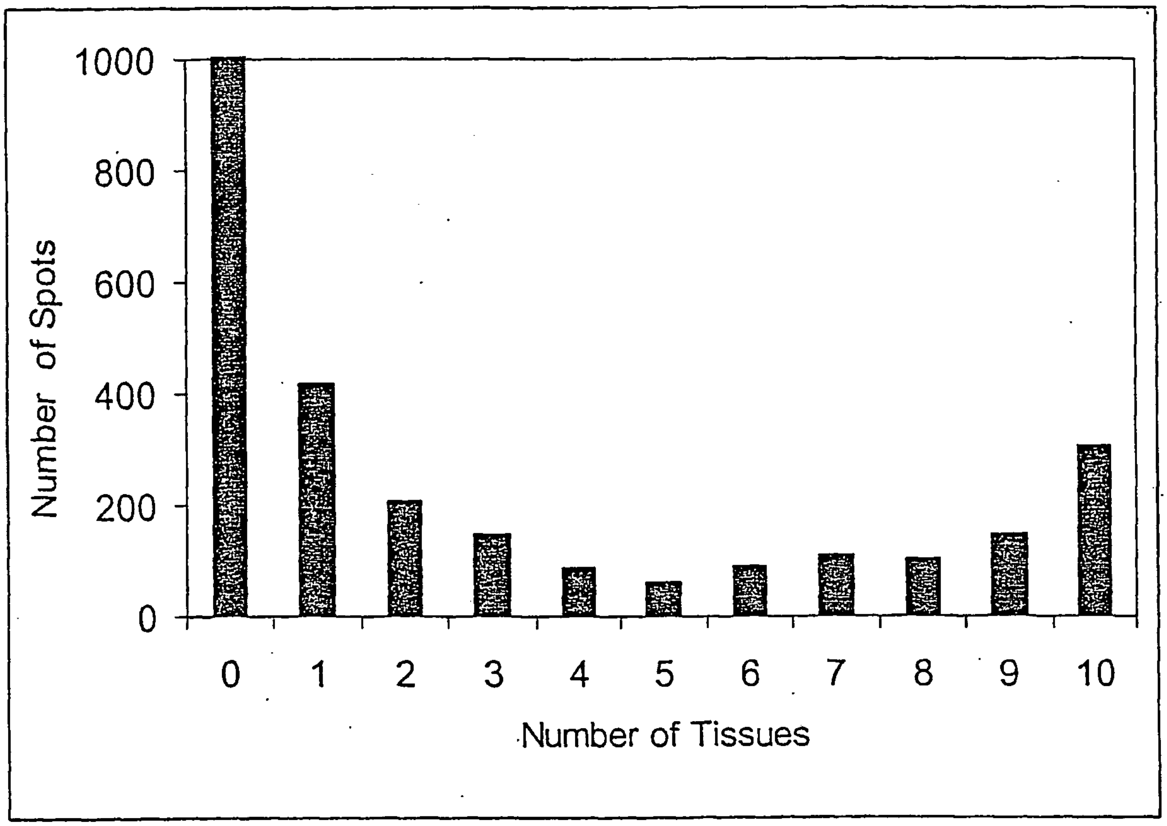
21 00
22 50
24 00
Length

Fig. 5



1000
800
600
400
200
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Number of Spots
0
1
2
3
4
5
6
7
8
9
10
Number of Tissues

Fig. 6

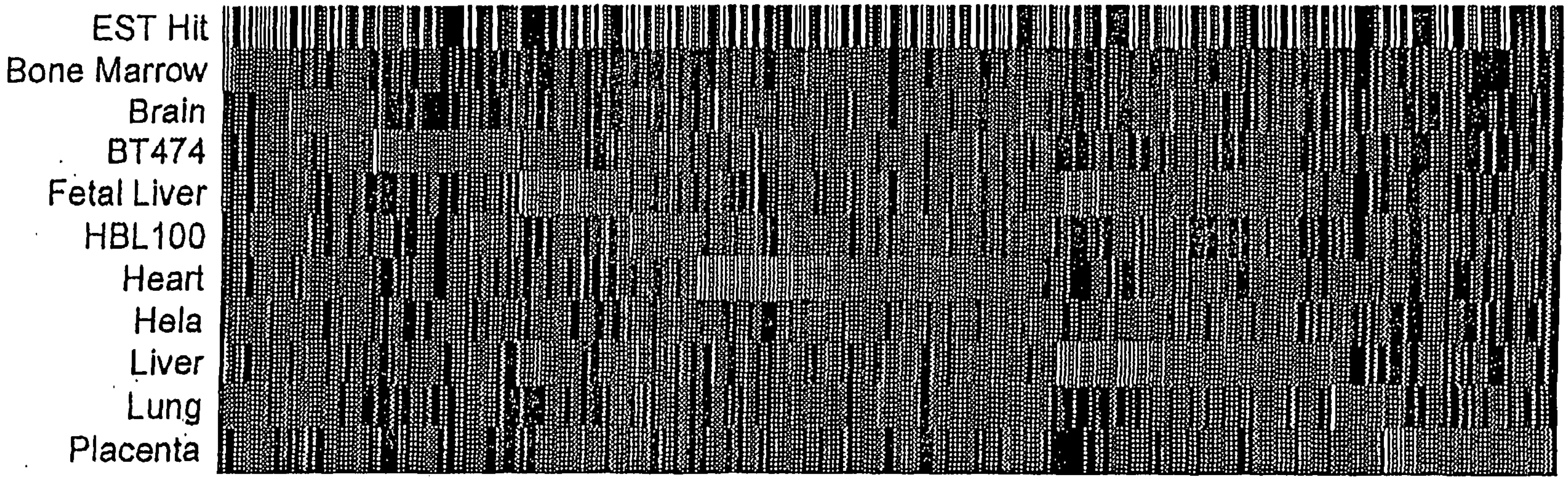


Fig. 7a

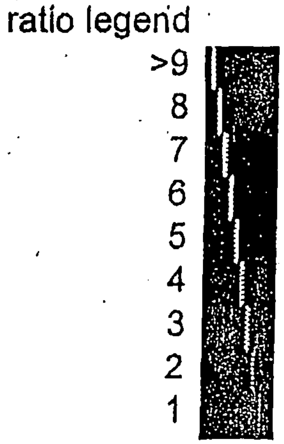


Fig. 7b

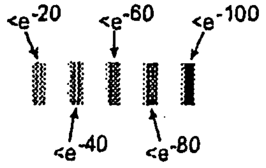
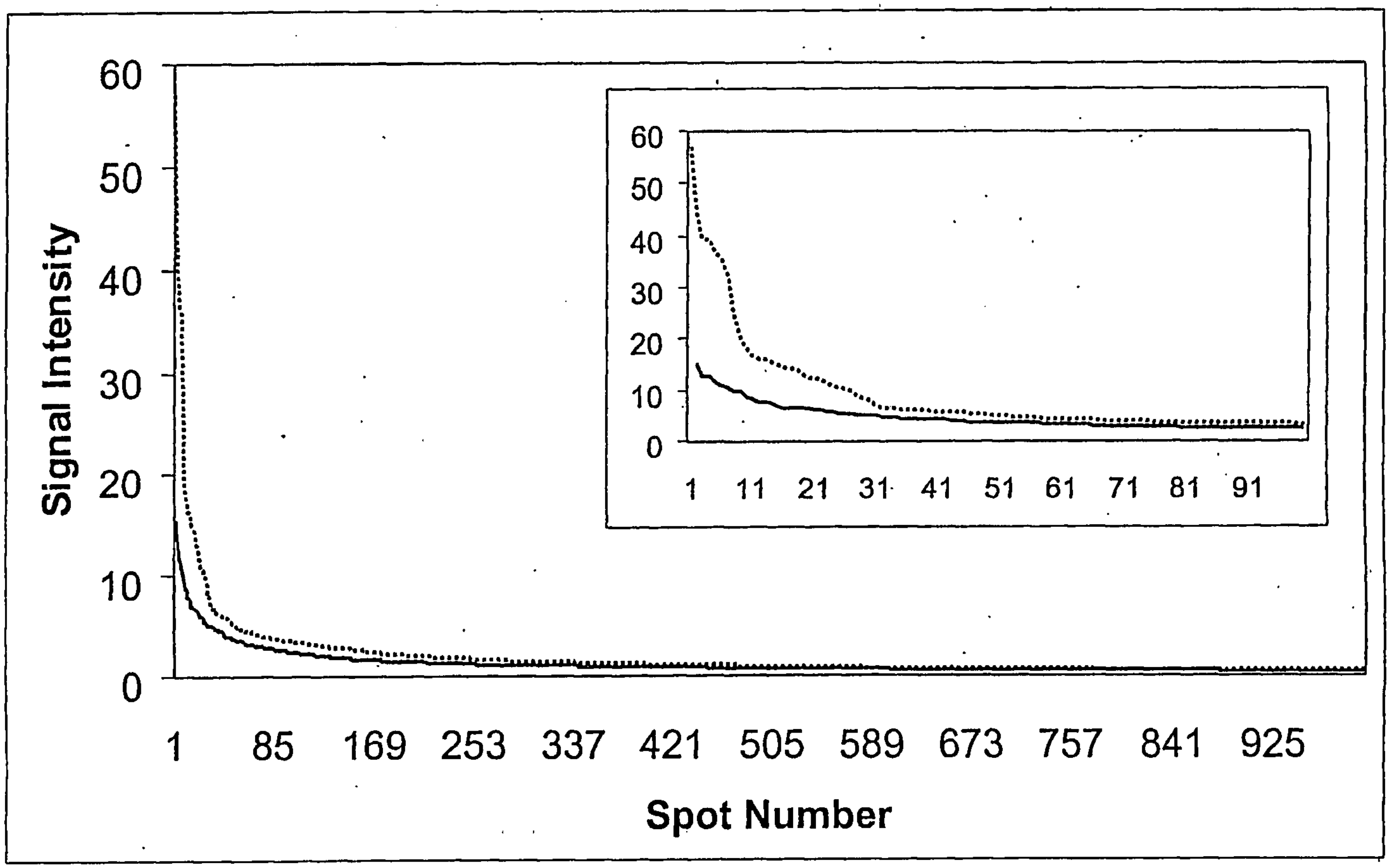


Fig. 7c


Signal Intensity
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50
40
30
20
10
0
1
85
169
253
337
421
505
589
673
757
841
925
Spot Number
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10
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21
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71
81
91

Fig. 8

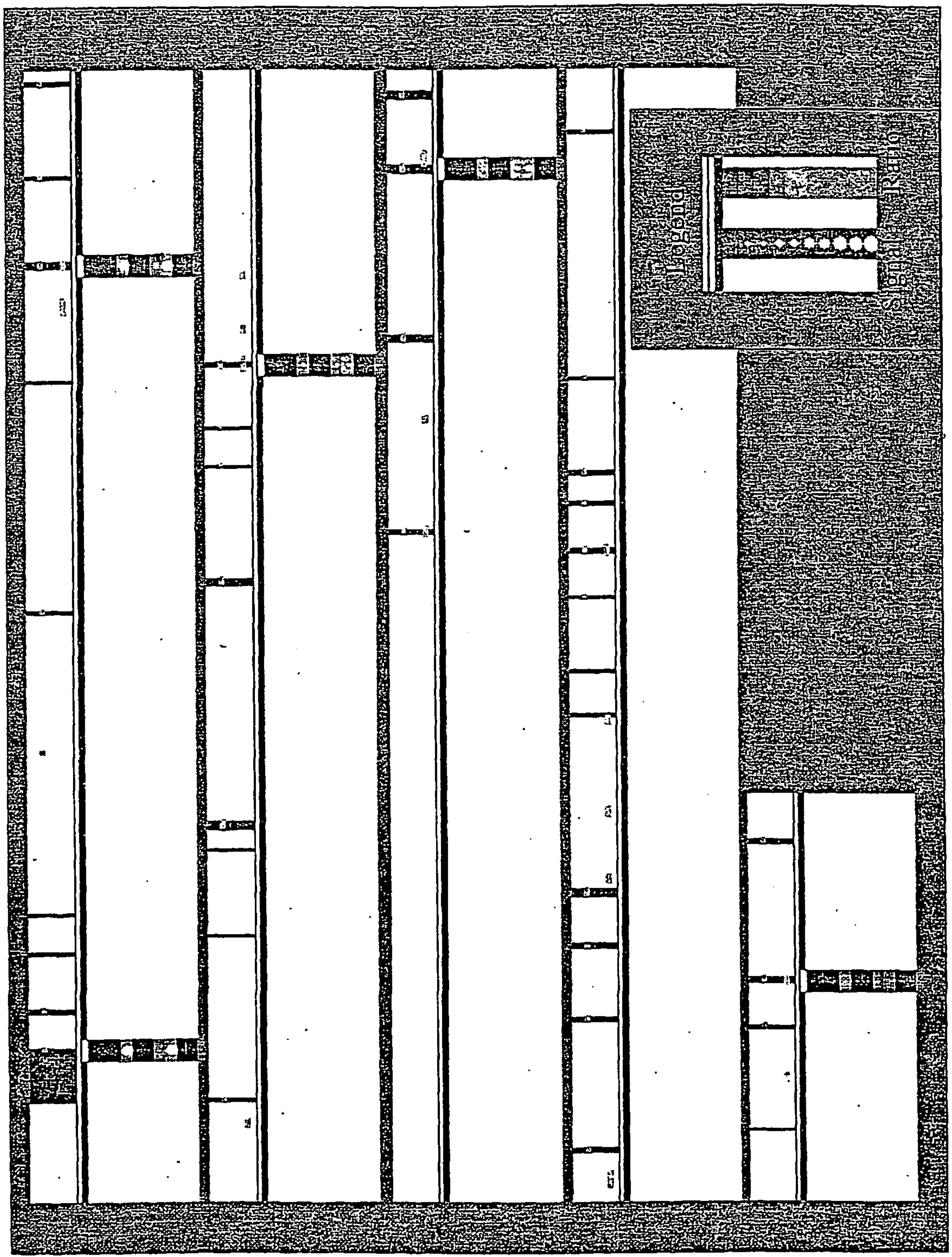

Fig. 9

Fig. 10